

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:02:07 ; Search time 16.5871 Seconds  
(without alignments)  
3219.466 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	925	100.0	361	3	AAY71385	Aay71385 Alternati
2	925	100.0	1163	3	AAY71310	Aay71310 Rat neuri
3	925	100.0	1163	3	AAY71384	Aay71384 Alternati
4	925	100.0	1163	5	ABB81074	Abb81074 Rat neuro
5	922	99.7	379	7	ADB85283	Adb85283 Rat fooce
6	921	99.6	199	5	ABB81077	Abb81077 Rat neuro
7	921	99.6	360	3	AAY71383	Aay71383 Rat neuri
8	921	99.6	360	5	ABB81076	Abb81076 Rat neuro
9	921	99.6	522	3	AAY71312	Aay71312 Rat neuri

10	919	99.4	199	3	AAAY71559	Aay71559	Rat	Nogo
11	919	99.4	359	3	AAAY71558	Aay71558	Rat	Nogo
12	919	99.4	403	3	AAAY71563	Aay71563	Rat	Nogo
13	919	99.4	1162	3	AAAY71557	Aay71557	Rat	Nogo
14	908	98.2	893	3	AAAY95012	Aay95012	Human	sec
15	908	98.2	983	6	ABU11573	Abu11573	Human	MDD
16	908	98.2	1178	3	AAAY71311	Aay71311	Human	neu
17	908	98.2	1192	3	AAAY56967	Aay56967	Human	MAG
18	908	98.2	1192	4	AAB82349	Aab82349	Human	NOG
19	908	98.2	1192	4	AAU04591	Aau04591	Human	Nog
20	908	98.2	1192	5	ABG30938	Abg30938	Human	Nog
21	908	98.2	1192	5	ABP68600	Abp68600	Human	pan
22	908	98.2	1192	5	ABB81078	Abb81078	Human	neu
23	908	98.2	1192	6	ABR59667	Abr59667	Human	Nog
24	905	97.8	200	4	AAB64514	Aab64514	Human	sec
25	904	97.7	199	2	AAW53947	Aaw53947	Human	NSP
26	904	97.7	199	2	AAW78313	Aaw78313	Fragment	
27	904	97.7	199	3	AAB12805	Aab12805	Human	NSP
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29	904	97.7	199	5	ABB81080	Abb81080	Human	neu
30	904	97.7	373	3	AAAY53624	Aay53624	A bone	ma
31	904	97.7	373	3	AAAY56969	Aay56969	Human	MAG
32	904	97.7	373	3	AAB24242	Aab24242	Human	Nog
33	904	97.7	373	4	AAB82350	Aab82350	Human	NOG
34	904	97.7	373	5	AAM47954	Aam47954	Human	RTN
35	904	97.7	373	5	ABG30937	Abg30937	Human	Nog
36	904	97.7	373	5	ABP68601	Abp68601	Human	pan
37	904	97.7	373	5	ABB81079	Abb81079	Human	neu
38	900	97.3	291	4	AAM93484	Aam93484	Human	pol
39	895	96.8	199	2	AAAY35903	Aay35903	Extended	
40	871.5	94.2	642	2	AAW58383	Aaw58383	Human	sec
41	871.5	94.2	642	4	AAB90682	Aab90682	Human	BG1
42	864	93.4	199	5	ABG30939	Abg30939	Human	Nog
43	828	89.5	175	2	AAW78194	Aaw78194	Human	sec
44	679	73.4	202	4	AAB64513	Aab64513	Gene	27 h
45	679	73.4	208	3	AAB12808	Aab12808	NSPC	prot

#### ALIGNMENTS

##### RESULT 1

AAAY71385

ID AAY71385 standard; protein; 361 AA.

XX

AC AAY71385;

XX

DT 02-NOV-2000 (first entry)

XX

DE Alternative version of rat neurite growth inhibitor Nogo B.

XX

KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT Region 1. .172  
FT /note= "Corresponds to amino acids 1-172 of Nogo A  
FT protein shown in AAY71310"  
FT Inhibitory-site 1. .171  
FT /note= "Inhibits NIH 3T3 fibroblast spreading"  
FT Modified-site 30  
FT /note= "Casein kinase II site"  
FT Region 31. .58  
FT /note= "Acidic region"  
FT Region 173. .361  
FT /note= "Corresponds to amino acids 975-1163 of Nogo A  
FT protein (AAY71310)"  
FT Region 174. .361  
FT /note= "This region is common to Nogo A, B and C  
FT isoforms"  
FT Domain 186. .221  
FT /label= Transmembrane\_domain  
FT /note= "C-terminal hydrophobic region"  
FT Modified-site 222  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 269. .271  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 271  
FT /note= "Protein kinase C (PKC) site"  
FT Modified-site 287  
FT /note= "Protein kinase C (PKC) site"  
FT Domain 288. .323  
FT /label= Transmembrane\_domain  
FT /note= "C-terminal hydrophobic region"  
FT Modified-site 339. .341  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 341  
FT /note= "Protein kinase C (PKC) site"  
XX  
PN WO200031235-A2.  
XX  
PD 02-JUN-2000.  
XX  
PF 05-NOV-1999; 99WO-US026160.  
XX  
PR 06-NOV-1998; 98US-0107446P.  
XX  
PA (SCHW/) SCHWAB M E.  
PA (CHEN/) CHEN M S.  
XX  
PI Schwab ME, Chen MS;  
XX  
DR WPI; 2000-400052/34.  
XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX

PS Claim 4; Page; 122pp; English.

XX

CC The present sequence is an alternative version of rat Nogo B protein  
CC which is a potent neural cell growth inhibitor and is free of all central  
CC nervous system (CNS) myelin material with which it is natively  
CC associated. The Nogo B transcript arises as a result of alternative  
CC splicing of Nogo gene. Nogo proteins and fragments displaying neurite  
CC growth inhibitory activity are used in the treatment of neoplastic  
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,  
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic  
CC neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma  
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's  
CC diseases. Therapeutics which promote Nogo activity can be used to treat  
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.  
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic  
CC acids can be used to inhibit production of Nogo protein to induce  
CC regeneration of neurons or to promote structural plasticity of the CNS in  
CC disorders where neurite growth, regeneration or maintenance are deficient  
CC or desired. The animal models can be used in diagnostic and screening  
CC methods for predisposition to disorders and to screen for or test  
CC molecules which can treat or prevent disorders or diseases of the CNS.  
CC Note: The present sequence is not given in the specification but is  
CC derived from Nogo A protein sequence (AAY71310) and corresponds to  
CC residues 1-172 fused to 975-1163 of Nogo A. This sequence is an  
CC alternative version of the Nogo B sequence (see AAY71383) described in  
CC the specification as being residues 1-172 fused to C-terminal 188 amino  
CC acids (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in  
CC claim 32 and SEQ ID NO: 29 in disclosure of the specification. However  
CC the specification does not include sequences for these SEQ ID numbers

XX

SQ Sequence 361 AA;

Query Match 100.0%; Score 925; DB 3; Length 361;

Best Local Similarity 100.0%; Pred. No. 8.7e-90;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA	60
Db	173	SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA	232
Qy	61	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV	120
Db	233	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV	292
Qy	121	LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	180
Db	293	LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	352
Qy	181	IPGLKRKAD	189
Db	353	IPGLKRKAD	361

RESULT 2

AAY71310

ID AAY71310 standard; protein; 1163 AA.

XX



AC AAY71310;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat neurite growth inhibitor Nogo A.  
 XX  
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Inhibitory-site 1. .171  
 FT /note= "Inhibits NIH 3T3 fibroblast spreading"  
 FT Modified-site 30  
 FT /note= "Casein kinase II site"  
 FT Region 31. .58  
 FT /note= "Acidic region"  
 FT Region 31. .57  
 FT /note= "Region specifically described in claim 16"  
 FT Region 172. .259  
 FT /note= "This region is not essential for inhibitory  
 FT activity"  
 FT Modified-site 233  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 242. .244  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 291  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 295  
 FT /note= "Protein kinase C (PKC) site"  
 FT Misc-difference 404  
 FT /note= "Encoded by TTG"  
 FT Modified-site 436  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 468. .470  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 484  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 488  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 502  
 FT /note= "Casein kinase II site"  
 FT Inhibitory-site 542. .722  
 FT Modified-site 576  
 FT /note= "Casein kinase II site"  
 FT Peptide 623. .640  
 FT /note= "used as immunogen to generate antibody AS 472"  
 FT Modified-site 626  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 694. .696  
 FT /note= "Asn is N-glycosylated"

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FT		/note= "Casein kinase II site"
FT	Peptide	762. .1163
FT		/note= "used as immunogen to generate antibody AS Bruna"
FT	Modified-site	784
FT		/note= "Protein kinase C (PKC) site"
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FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	863
FT		/note= "Casein kinase II site"
FT	Modified-site	868
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	893
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	912. .914
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	925. .927
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	954
FT		/note= "PKC and casein kinase II sites"
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FT		/note= "PKC and casein kinase II sites"
FT	Region	975. .1162
FT		/note= "This region is not essential for inhibitory activity"
FT	Region	976. .1163
FT		/note= "C-terminal common region found in Nogo A, B and C isoforms"
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FT		/label= Transmembrane_domain
FT		/note= "C-terminal hydrophobic region specifically described in claim 16"
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FT		/note= "Asn is N-glycosylated"
FT	Modified-site	1073
FT		/note= "Protein kinase C (PKC) site"
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FT		/note= "Protein kinase C (PKC) site"
FT	Domain	1090. .1125
FT		/label= Transmembrane_domain
FT		/note= "C-terminal hydrophobic region specifically described in claim 16"
FT	Modified-site	1141. .1143
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FT	Modified-site	1143
FT		/note= "Protein kinase C (PKC) site"
XX		
PN	WO200031235-A2.	
XX		
PD	02-JUN-2000.	
XX		

XX

XX

PA

PA

XX

PI

XX

DR

DR

XX

PT

PT

XX

PS

XX

CC

XX

SO

### Query Match

100.0%; Score 925; DB 3; Length 1163;

## Best Local Similarity

100.0%: Pred. No. 4e-89:

Matches 189; Conservative

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0; Mismatches      0
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Indels 0:

Gaps 0:

QY

1 SVVDLLYWRDIKKTGVVFGASLFLILLSLTVFSIVSVTAYIALALLSVTISERIYKGVIOA 60

|||||

Db

975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIOA 1034

Qy

61 IOKSDEGHPPFRAYLESEVAISEFELVOKYSNSALGHVNSTIKELBRIELVDDLVDSIKFAY 120

|||||

Db 1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKFV 1094

QY 121 LMWVFYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1095 LMWVFYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154

QY 181 IPGLKRRKAD 189  
 ||||||||

Db 1155 IPGLKRRKAD 1163

RESULT 3

AA71384

ID AAY71384 standard; protein; 1163 AA.

XX

AC AAY71384;

XX

DT 02-NOV-2000 (first entry)

XX

DE Alternative version of rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Inhibitory-site 1. .171

FT /note= "Inhibits NIH 3T3 fibroblast spreading"

FT Modified-site 30

FT /note= "Casein kinase II site"

FT Region 31. .58

FT /note= "Acidic region"

FT Region 172. .259

FT /note= "This region is not essential for inhibitory activity"

FT Misc-difference 223

FT /label= Unknown

FT /note= "There is Leu at this position in the sequence shown in AAY71310"

FT Modified-site 233

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 242. .244

FT /note= "Asn is N-glycosylated"

FT Modified-site 291

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 295

FT /note= "Protein kinase C (PKC) site"

FT Misc-difference 404

FT /note= "There is Ile at this position in the sequence shown in AAY71310"

FT Modified-site 436

FT		/note= "Protein kinase C (PKC) site"
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FT	Modified-site	502
FT		/note= "Casein kinase II site"
FT	Inhibitory-site	542. .722
FT	Modified-site	576
FT		/note= "Casein kinase II site"
FT	Peptide	623. .640
FT		/note= "used as immunogen to generate antibody AS 472"
FT	Modified-site	626
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FT		/note= "There is Asn at this position in the sequence shown in AAY71310"
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FT	Modified-site	715
FT		/note= "Casein kinase II site"
FT	Peptide	762. .1163
FT		/note= "used as immunogen to generate antibody AS Bruna"
FT	Modified-site	784
FT		/note= "Protein kinase C (PKC) site"
FT	Misc-difference	820
FT		/note= "There is Leu at this position in the sequence shown in AAY71310"
FT	Modified-site	821
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	863
FT		/note= "Casein kinase II site"
FT	Modified-site	868
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	893
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	912. .914
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	925. .927
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	954
FT		/note= "PKC and casein kinase II sites"
FT	Modified-site	956
FT		/note= "PKC and casein kinase II sites"
FT	Region	975. .1162
FT		/note= "This region is not essential for inhibitory activity"

FT Region 976. .1163  
 FT /note= "C-terminal common region found in Nogo A, B and C  
 FT isoforms"  
 FT Domain 988. .1023  
 FT /label= Transmembrane\_domain  
 FT /note= "C-terminal hydrophobic region"  
 FT Modified-site 1024  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 1071. .1073  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 1073  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 1089  
 FT /note= "Protein kinase C (PKC) site"  
 FT Domain 1090. .1125  
 FT /label= Transmembrane\_domain  
 FT /note= "C-terminal hydrophobic region"  
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 FT /note= "Asn is N-glycosylated"  
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 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Claim 3; Fig 13; 122pp; English.  
 XX  
 CC The present sequence is an alternative version of rat Nogo A protein  
 CC which is a potent neural cell growth inhibitor and is free of all central  
 CC nervous system (CNS) myelin material with which it is natively  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The



1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60



Db 975 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1034  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 Db 1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1094  
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 Db 1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154  
 Qy 181 IPGLKRKAD 189  
 Db 1155 IPGLKRKAD 1163

RESULT 5

ADB85283

ID ADB85283 standard; protein; 379 AA.

XX

AC ADB85283;

XX

DT 04-DEC-2003 (first entry)

XX

DE Rat foocen-m2 reticulon SEQ ID NO:164.

XX

KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;  
 KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;  
 KW protease; enzyme; analgesic; gene therapy; pain; diabetes.

XX

OS Rattus norvegicus.

XX

PN EP1284297-A2.

XX

PD 19-FEB-2003.

XX

PF 26-JUL-2002; 2002EP-00255228.

XX

PR 27-JUL-2001; 2001GB-00018354.

PR 07-FEB-2002; 2002GB-00002880.

XX

PA (WARN ) WARNER LAMBERT CO.

XX

PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

XX

DR WPI; 2003-364994/35.

DR N-PSDB; ADB85284.

XX

PT Use of gene sequence that is down-regulated in response to streptozocin-  
 PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in  
 PT screening of compounds for treating or diagnosing pain.

XX

PS Disclosure; Page 239-240; 256pp; English.

XX

CC The invention relates to a novel isolated gene sequence that is down-  
 CC regulated in the spinal cord in response to streptozocin-induced  
 CC diabetes, or comprising, hybridising or having at least 80% sequence  
 CC identity to a sequence whose expression products are kinases,

CC phosphatases, ion channel proteins, receptors, transporters, G-protein  
 CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,  
 CC given in the specification. A gene of the invention has analgesic  
 CC activity, and may have a use in gene therapy. The gene sequences, vector,  
 CC host cell, animal, polypeptide and antibody are useful for screening of  
 CC compounds for diagnosing or treating pain. The kits are useful for  
 CC simultaneous, separate or sequential detecting and/or quantifying down-  
 CC regulation of a gene sequence in the spinal cord of a mammal in response  
 CC to streptozocin-induced diabetes. The compound or pharmaceutical  
 CC composition is useful as a medicament for treating or diagnosing pain.  
 CC The present sequence represents a protein encoded by a gene of the  
 CC invention.  
 XX  
 SQ Sequence 379 AA;

Query Match 99.7%; Score 922; DB 7; Length 379;  
 Best Local Similarity 99.5%; Pred. No. 1.9e-89;  
 Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SVVDLLYWDRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA	60
		:	
Db	191	AVVDLLYWDRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA	250
Qy	61	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV	120
Db	251	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV	310
Qy	121	LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	180
Db	311	LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	370
Qy	181	IPGLKRRKAD	189
Db	371	IPGLKRRKAD	379

# RESULT 6

ABB81077

ID ABB81077 standard; protein; 199 AA.

XX

AC ABB81077;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-C.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;  
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.  
 XX  
 PF 28-JUN-2001; 2001US-00893348.  
 XX  
 PR 19-MAY-1998; 98IL-00124500.  
 PR 21-JUL-1998; 98WO-US014715.  
 PR 22-DEC-1998; 98US-00218277.  
 PR 19-MAY-1999; 99US-00314161.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;  
 PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR N-PSDB; ABN86600.  
 XX  
 PT Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.  
 XX  
 PS Example 5; Page 48-49; 93pp; English.  
 XX  
 CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-C, an example of NS-specific  
 CC antigen  
 XX  
 SQ Sequence 199 AA;

Query Match

99.6%; Score 921; DB 5; Length 199;

Best Local Similarity 100.0%; Pred. No. 1.1e-89;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61
         |||
Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 71

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLQFAVL 121
         |||
Db      72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLQFAVL 131

Qy      122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
         |||
Db      132 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 191

Qy      182 PGLKRKAD 189
         |||
Db      192 PGLKRKAD 199

```

# RESULT 7

AAAY71383

ID AAY71383 standard; protein; 360 AA.

XX

AC AAY71383;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo B.

XX

KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Region 1. .172

FT /note= "Corresponds to amino acids 1-172 of Nogo A  
protein shown in AAY71310"

FT Inhibitory-site 1. .171

FT /note= "Inhibits NIH 3T3 fibroblast spreading"

FT Modified-site 30

FT /note= "Casein kinase II site"

FT Region 31. .58

FT /note= "Acidic region"

FT Region 173. .360

FT /note= "Corresponds to C-terminal 188 amino acids  
(residues 976-1163) of Nogo A protein (AAY71310). This  
region is common to Nogo A, B and C isoforms"

FT Domain 185. .220

FT /label= Transmembrane\_domain

FT /note= "C-terminal hydrophobic region"

FT Modified-site 221  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 268. .270  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 270  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 286  
 FT /note= "Protein kinase C (PKC) site"  
 FT Domain 287. .322  
 FT /label= Transmembrane\_domain  
 FT /note= "C-terminal hydrophobic region"  
 FT Modified-site 338. .340  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 340  
 FT /note= "Protein kinase C (PKC) site"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Example; Page; 122pp; English.  
 XX  
 CC The present sequence is a rat Nogo B protein which is a potent neural  
 CC cell growth inhibitor and is free of all central nervous system (CNS)  
 CC myelin material with which it is natively associated. The Nogo B  
 CC transcript arises as a result of alternative splicing of Nogo gene. Nogo  
 CC proteins and fragments displaying neurite growth inhibitory activity are  
 CC used in the treatment of neoplastic disease of the CNS e.g. glioma,  
 CC glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
 CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,  
 CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
 CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
 CC activity can be used to treat or prevent hyperproliferative or benign  
 CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
 CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
 CC production of Nogo protein to induce regeneration of neurons or to  
 CC promote structural plasticity of the CNS in disorders where neurite  
 CC growth, regeneration or maintenance are deficient or desired. The animal  
 CC models can be used in diagnostic and screening methods for predisposition  
 CC to disorders and to screen for or test molecules which can treat or  
 CC prevent disorders or diseases of the CNS. Note: The present sequence is  
 CC not given in the specification but is derived from Nogo A protein  
 CC sequence (AAY71310) and corresponds to residues 1-172 fused to 976-1163

CC of Nogo A. The specification claims an alternative version of this  
 CC sequence (see AAY71385.) which corresponds to residues 1-172 fused to 975  
 CC -1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID  
 CC NO: 29 in disclosure of the specification. However the specification does  
 CC not include sequences for these SEQ ID numbers  
 XX  
 SQ Sequence 360 AA;

Query Match 99.6%; Score 921; DB 3; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-89;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI	61
Db	173	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI	232
QY	62	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKLFAVL	121
Db	233	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKLFAVL	292
QY	122	MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	181
Db	293	MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	352
QY	182	PGLKRKAD	189
Db	353	PGLKRKAD	360

# RESULT 8

ABB81076

ID ABB81076 standard; protein; 360 AA.

XX

AC ABB81076;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-B.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

KW central nervous system; peripheral nervous system; tranquillizer; Nogo;

KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;

KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 XX  
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;  
 PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR N-PSDB; ABN86600.  
 XX  
 PT Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.  
 XX  
 PS Example 5; Page 47-48; 93pp; English.  
 XX  
 CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-B, an example of NS-specific  
 CC antigen  
 XX  
 SQ Sequence 360 AA;

Query Match 99.6%; Score 921; DB 5; Length 360;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-89;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 232

Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLQKFAVL 121  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLQKFAVL 292  
 Qy 122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 293 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352  
 Qy 182 PGLKRRKAD 189  
 |||||||  
 Db 353 PGLKRRKAD 360

RESULT 9

AAAY71312

ID AAY71312 standard; protein; 522 AA.

XX

AC AAY71312;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo C.

XX

KW Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Region

1. .39

FT /note= "Sequence upstream to the N-terminus of Nogo C  
 FT protein"

FT Misc-difference 3

FT /note= "Encoded by TAG"

FT Region

11. .191

FT /note= "Region specifically described in claim 16"

FT Misc-difference 29

FT /note= "Encoded by TAA"

FT Protein

40. .238

FT /label= Nogo\_C\_protein

FT Region

51. .238

FT /note= "C-terminal common region found in Nogo A, B and C  
 FT isoforms "

FT Region

239. .522

FT /note= "Sequence downstream to the C-terminus of Nogo C  
 FT protein"

FT Misc-difference 239

FT /note= "Encoded by TGA"

FT Misc-difference 263

FT /note= "Encoded by TGA"

FT Misc-difference 276

FT /note= "Encoded by TAG"



FT Misc-difference 281  
 FT /note= "Encoded by TGA"  
 FT Misc-difference 295  
 FT /note= "Encoded by TAA"  
 FT Misc-difference 298  
 FT /note= "Encoded by TAA"  
 FT Misc-difference 314  
 FT /note= "Encoded by TGA"  
 FT Misc-difference 318  
 FT /note= "Encoded by TGA"  
 FT Misc-difference 335  
 FT /note= "Encoded by TAG"  
 FT Misc-difference 371  
 FT /note= "Encoded by TGA"  
 FT Misc-difference 374  
 FT /note= "Encoded by TAG"  
 FT Misc-difference 380  
 FT /note= "Encoded by TAA"  
 FT Misc-difference 406  
 FT /note= "Encoded by TAA"  
 FT Misc-difference 408  
 FT /note= "Encoded by TAG"  
 FT Misc-difference 410  
 FT /note= "Encoded by TAA"  
 FT Misc-difference 422  
 FT /note= "Encoded by TAA"  
 FT Misc-difference 433  
 FT /note= "Encoded by TGA"  
 FT Misc-difference 440  
 FT /note= "Encoded by TAG"  
 FT Misc-difference 453  
 FT /note= "Encoded by TAG"  
 FT Misc-difference 465  
 FT /note= "Encoded by TAG"  
 FT Misc-difference 482  
 FT /note= "Encoded by TAG"  
 FT Misc-difference 513  
 FT /note= "Encoded by TAA"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 DR N-PSDB; AAD01175.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.

XX  
 PS Claim 7; Fig 14; 122pp; English.  
 XX  
 CC The present sequence is a rat Nogo C protein which is a potent neural  
 CC cell growth inhibitor and is free of all central nervous system (CNS)  
 CC myelin material with which it is natively associated. Nogo proteins and  
 CC fragments displaying neurite growth inhibitory activity are used in the  
 CC treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
 CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
 CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma,  
 CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
 CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
 CC activity can be used to treat or prevent hyperproliferative or benign  
 CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
 CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
 CC production of Nogo protein to induce regeneration of neurons or to  
 CC promote structural plasticity of the CNS in disorders where neurite  
 CC growth, regeneration or maintenance are deficient or desired. The animal  
 CC models can be used in diagnostic and screening methods for predisposition  
 CC to disorders and to screen for or test molecules which can treat or  
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
 CC specification. However the specification does not include sequences for  
 CC these SEQ ID numbers  
 XX  
 SQ Sequence 522 AA;

Query Match 99.6%; Score 921; DB 3; Length 522;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-89;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 51 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 110  
 Qy 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 111 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 170  
 Qy 122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 171 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 230  
 Qy 182 PGLKRKAD 189  
 ||||||||  
 Db 231 PGLKRKAD 238

RESULT 10

AAY71559

ID AAY71559 standard; protein; 199 AA.

XX

AC AAY71559;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C.

XX  
 KW Rat; neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .11  
 FT /note= "Corresponds to residues 40-50 of rat Nogo C  
 FT protein shown in AAY71312"  
 FT Region 12. .199  
 FT /note= "Corresponds to residues 975-1162 of rat Nogo A  
 FT protein shown in AAY71310"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Example; Page; 122pp; English.  
 XX  
 CC The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is natively  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, menangioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can  
 CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is derived by fusing two fragments from rat Nogo C and Nogo A proteins.

CC The fragment is used in the construction of mutant Nogo-C which is  
 CC composed of His-tag/T7-tag/Nogo-C N-terminus (11 aa) + Nogo-A sequence aa  
 CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory  
 CC sites of Nogo protein. Major inhibitory region was identified in the Nogo  
 CC A sequence from amino acids 172-974, particularly amino acids 542-722. In  
 CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3  
 CC fibroblast spreading. Note: The present sequence is not given in the  
 CC specification but is derived from rat Nogo C sequence shown in AAY71312  
 CC and Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred  
 CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.  
 CC However, the specification does not include sequences for these SEQ ID  
 CC numbers  
 XX  
 SQ Sequence 199 AA;

Query Match 99.4%; Score 919; DB 3; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-89;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA	60
Db	12	SVVDLLYWRIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA	71
Qy	61	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV	120
Db	72	IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV	131
Qy	121	LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	180
Db	132	LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK	191
Qy	181	IPGLKRKA	188
Db	192	IPGLKRKA	199

# RESULT 11

AAY71558

ID AAY71558 standard; protein; 359 AA.

XX

AC AAY71558;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A protein fragment used in the construction of mutant Nogo-B.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Region 1. .171  
 FT /note= "Corresponds to residues 1-171 of rat Nogo A  
 FT protein shown in AAY71310"  
 FT Region 172. .359  
 FT /note= "Corresponds to residues 975-1162 of rat Nogo A  
 FT protein shown in AAY71310"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Example; Page; 122pp; English.  
 XX  
 CC The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is natively  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can  
 CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is derived by fusing two fragments of rat Nogo A protein shown in  
 CC AAY71310. The fragment is used in the construction of mutant Nogo-B. The  
 CC mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +  
 CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory  
 CC sites of Nogo protein. Major inhibitory region was identified in the Nogo  
 CC A sequence from amino acids 172-974, particularly amino acids 542-722. In  
 CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3  
 CC fibroblast spreading. Note: The present sequence is not given in the  
 CC specification but is derived from rat Nogo A sequence shown in AAY71310.  
 CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in  
 CC disclosure of the specification. However, the specification does not  
 CC include sequences for these SEQ ID numbers  
 XX

SQ Sequence 359 AA;

Query Match 99.4%; Score 919; DB 3; Length 359;  
Best Local Similarity 100.0%; Pred. No. 3.8e-89;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
          |||
Db      172 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 231

Qy      61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120
          |||
Db      232 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 291

Qy      121 LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
          |||
Db      292 LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 351

Qy      181 IPGLKRKA 188
          |||
Db      352 IPGLKRKA 359
```

RESULT 12

AA71563

ID AAY71563 standard; protein; 403 AA.

XX

AC AAY71563;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A protein fragment used in the construction of mutant EST.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.

XX  
PS Example; Page; 122pp; English.  
XX

CC The patent relates to neurite growth inhibitor Nogo which is free of all  
CC central nervous system (CNS) myelin material with which it is natively  
CC associated. Nogo proteins and fragments displaying neurite growth  
CC inhibitory activity are used in the treatment of neoplastic disease of  
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and  
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
CC Therapeutics which promote Nogo activity can be used to treat or prevent  
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
CC used to inhibit production of Nogo protein to induce regeneration of  
CC neurons or to promote structural plasticity of the CNS in disorders where  
CC neurite growth, regeneration or maintenance are deficient or desired. The  
CC animal models can be used in diagnostic and screening methods for  
CC predisposition to disorders and to screen for or test molecules which can  
CC treat or prevent disorders or diseases of the CNS. The present sequence  
CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in  
CC the construction of mutant EST. The mutant is composed of His-tag/T7-  
CC tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for  
CC mapping the inhibitory sites of Nogo protein. Major inhibitory region was  
CC identified in the Nogo A sequence from amino acids 172-974, particularly  
CC amino acids 542-722. In addition, N-terminal region 1-171 was found to be  
CC inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is  
CC not given in the specification but is derived from rat Nogo A sequence  
CC shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ  
CC ID NO: 29 in disclosure of the specification. However, the specification  
CC does not include sequences for these SEQ ID numbers

XX  
SQ Sequence 403 AA;

Query Match 99.4%; Score 919; DB 3; Length 403;  
Best Local Similarity 100.0%; Pred. No. 4.4e-89;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQA 60  
|  
Db 216 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQA 275  
  
Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
|  
Db 276 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 335  
  
Qy 121 LMWVFETYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVK DAMAKI QAK 180  
|  
Db 336 LMWVFETYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVK DAMAKI QAK 395  
  
Qy 181 IPGLKRKA 188  
|  
Db 396 IPGLKRKA 403

RESULT 13

AA71557

ID AA71557 standard; protein; 1162 AA.

XX

AC AA71557;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.

XX

PS Example; Page; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is natively  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can



CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is a truncated form of rat Nogo A protein shown in AAY71310, which is  
 CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-  
 CC tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were  
 CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory  
 CC region was identified in the Nogo A sequence from amino acids 172-974,  
 CC particularly amino acids 542-722. In addition, N-terminal region 1-171  
 CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The  
 CC present sequence is not given in the specification but is derived from  
 CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred  
 CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.  
 CC However, the specification does not include sequences for these SEQ ID  
 CC numbers  
 XX  
 SQ Sequence 1162 AA;

Query Match 99.4%; Score 919; DB 3; Length 1162;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-88;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60  
 |||  
 Db 975 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1034  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 |||  
 Db 1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1094  
 Qy 121 LMWVFYVGALEFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 |||  
 Db 1095 LMWVFYVGALEFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154  
 Qy 181 IPGLKRKA 188  
 |||  
 Db 1155 IPGLKRKA 1162

# RESULT 14

AAAY95012

ID AAY95012 standard; protein; 893 AA.

XX

AC AAY95012;

XX

DT 19-JUN-2000 (first entry)

XX

DE Human secreted protein vb22\_1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;

KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;

KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;

KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX

PN WO200011015-A1.

XX

PD 02-MAR-2000.

XX  
 PF 24-AUG-1999; 99WO-US019351.  
 XX  
 PR 24-AUG-1998; 98US-0097638P.  
 PR 24-AUG-1998; 98US-0097659P.  
 PR 09-SEP-1998; 98US-0099618P.  
 PR 28-SEP-1998; 98US-0102092P.  
 PR 25-NOV-1998; 98US-0109978P.  
 PR 23-DEC-1998; 98US-0113645P.  
 PR 23-DEC-1998; 98US-0113646P.  
 PR 23-AUG-1999; 99US-00379246.  
 XX  
 PA (ALPH-) ALPHAGENE INC.  
 XX  
 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
 XX  
 DR WPI; 2000-224657/19.  
 XX  
 PT New secreted or transmembrane proteins and polynucleotides encoding them,  
 PT useful for treating neurodegenerative disorders, autoimmune diseases and  
 PT cancer.  
 XX  
 PS Claim 73; Page 322-325; 357pp; English.  
 XX  
 CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),  
 CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins  
 CC of the invention include those that are thought to be only partially  
 CC secreted, i.e., transmembrane proteins. The proteins of the invention may  
 CC exhibit one or more activities selected from the following: cytokine  
 CC activity; cell proliferation; differentiation; immune modulation;  
 CC haematopoiesis regulation; tissue growth activity; activin/inhibin  
 CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
 CC activity; anti-inflammatory activity; and tumour inhibition activity. The  
 CC proteins may be administered to patients as vaccines, and the nucleotides  
 CC may be used as part of a gene therapy regime. Diseases or conditions that  
 CC may be treated using the proteins or nucleotides of the invention include  
 CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
 CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
 CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
 CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
 CC allergic reactions such as asthma and anaemia. They may also be used for  
 CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
 CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
 CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
 CC activity may additionally be useful as contraceptives. Nucleic acid  
 CC sequences of the invention may be used in chromosome mapping, and as a  
 CC source of diagnostic primers and probes. The present sequence represents  
 CC one of the 40 proteins of the invention  
 XX  
 SQ Sequence 893 AA;

Query Match 98.2%; Score 908; DB 3; Length 893;  
 Best Local Similarity 97.4%; Pred. No. 1.8e-87;  
 Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60  
 |||

Db 705 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 764

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 |||

Db 765 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 824

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 |||

Db 825 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 884

Qy 181 IPGLKRKAD 189  
 |||

Db 885 IPGLKRKAE 893

# RESULT 15

ABU11573

ID ABU11573 standard; protein; 983 AA.

XX

AC ABU11573;

XX

DT 12-FEB-2003 (first entry)

XX

DE Human MDDT polypeptide SEQ ID 520.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;  
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;  
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;  
 KW gene therapy; protein replacement therapy; cell proliferative disorder;  
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
 KW psoriasis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO200279449-A2.

XX

PD 10-OCT-2002.

XX

PF 27-MAR-2002; 2002WO-US009944.

XX

PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-0300001P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX  
 DR WPI; 2003-058431/05.  
 DR N-PSDB; ABX34563.  
 XX  
 PT New purified disease detection and treatment molecule proteins and  
 PT polynucleotides, useful for diagnosing, treating or preventing cancers  
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis  
 PT or hepatitis.  
 XX  
 PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.  
 XX  
 CC This invention describes a novel disease detection and treatment molecule  
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,  
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides  
 CC and the polypeptides of the invention can be used for gene therapy,  
 CC protein replacement therapy and are useful for treating a variety of  
 CC diseases or conditions. These polypeptides or polynucleotides are  
 CC particularly useful for diagnosing, treating or preventing cell  
 CC proliferative disorders (e.g. cancers including adenocarcinoma,  
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded  
 CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 983 AA;

Query Match 98.2%; Score 908; DB 6; Length 983;  
 Best Local Similarity 97.4%; Pred. No. 2.1e-87;  
 Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60  
 |  
 Db 795 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 854  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 |  
 Db 855 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 914  
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 |  
 Db 915 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 974  
 Qy 181 IPGLKRKAD 189  
 |  
 Db 975 IPGLKRKAE 983

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 Job time : 17.5871 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:09:33 ; Search time 4.69196 Seconds  
 (without alignments)  
 2079.581 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
 Perfect score: 925  
 Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
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 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	904	97.7	199	2	US-08-700-607-1	Sequence 1, Appli
2	679	73.4	208	2	US-08-700-607-7	Sequence 7, Appli
3	679	73.4	356	2	US-08-700-607-6	Sequence 6, Appli
4	679	73.4	776	2	US-08-700-607-5	Sequence 5, Appli
5	665	71.9	267	2	US-08-700-607-8	Sequence 8, Appli
6	539.5	58.3	168	4	US-09-149-476-563	Sequence 563, App
7	516	55.8	241	2	US-08-700-607-3	Sequence 3, Appli
8	286	30.9	92	4	US-09-149-476-411	Sequence 411, App
9	100	10.8	80	3	US-08-905-223-411	Sequence 411, App
10	95	10.3	468	4	US-08-487-596-8	Sequence 8, Appli
11	95	10.3	468	4	US-08-660-451A-8	Sequence 8, Appli

12	88.5	9.6	1278	4	US-09-462-136-2	Sequence 2, Appli
13	86.5	9.4	592	4	US-09-134-000C-5477	Sequence 5477, Ap
14	86	9.3	414	4	US-08-956-171E-5246	Sequence 5246, Ap
15	85.5	9.2	1051	4	US-09-134-001C-5005	Sequence 5005, Ap
16	84.5	9.1	593	4	US-09-328-352-4866	Sequence 4866, Ap
17	82	8.9	614	4	US-09-540-236-2858	Sequence 2858, Ap
18	81.5	8.8	280	4	US-09-543-681A-6175	Sequence 6175, Ap
19	81	8.8	744	4	US-09-785-381-1	Sequence 1, Appli
20	81	8.8	744	4	US-09-785-381-3	Sequence 3, Appli
21	80.5	8.7	598	2	US-08-853-659A-53	Sequence 53, Appl
22	79	8.5	289	4	US-09-540-236-2019	Sequence 2019, Ap
23	79	8.5	554	4	US-09-252-991A-27968	Sequence 27968, A
24	78.5	8.5	748	3	US-09-061-764A-19	Sequence 19, Appl
25	78	8.4	231	4	US-09-198-452A-419	Sequence 419, App
26	78	8.4	420	4	US-09-134-001C-3805	Sequence 3805, Ap
27	78	8.4	424	4	US-09-543-681A-7510	Sequence 7510, Ap
28	78	8.4	970	4	US-09-795-927-7	Sequence 7, Appli
29	78	8.4	1053	4	US-09-328-352-5058	Sequence 5058, Ap
30	77.5	8.4	492	4	US-09-134-000C-4808	Sequence 4808, Ap
31	77	8.3	154	1	US-08-366-783-5	Sequence 5, Appli
32	77	8.3	292	4	US-09-489-039A-12212	Sequence 12212, A
33	77	8.3	720	4	US-09-134-000C-5631	Sequence 5631, Ap
34	76.5	8.3	601	4	US-09-134-000C-5783	Sequence 5783, Ap
35	76	8.2	700	4	US-09-543-681A-4969	Sequence 4969, Ap
36	76	8.2	993	4	US-08-836-687B-30	Sequence 30, Appl
37	75.5	8.2	231	4	US-09-724-623-116	Sequence 116, App
38	75.5	8.2	408	4	US-09-107-532A-6198	Sequence 6198, Ap
39	75.5	8.2	444	4	US-09-543-681A-5355	Sequence 5355, Ap
40	75.5	8.2	454	4	US-09-904-615-165	Sequence 165, App
41	75.5	8.2	501	4	US-09-328-352-5227	Sequence 5227, Ap
42	75.5	8.2	613	4	US-09-107-532A-6935	Sequence 6935, Ap
43	75	8.1	871	4	US-09-255-829-2	Sequence 2, Appli
44	75	8.1	871	4	US-09-255-829-8	Sequence 8, Appli
45	75	8.1	871	4	US-09-255-829-26	Sequence 26, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

##### ; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

##### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-1

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Query Match          97.7%; Score 904; DB 2; Length 199;
Best Local Similarity 97.3%; Pred. No. 5.7e-89;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 71

QY      62 QKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY      122 MWVFETYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
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QY      182 PGLKRKAD 189
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Db      192 PGLKRKAE 199

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RESULT 2

US-08-700-607-7

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; Sequence 7, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.

```

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; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307311
US-08-700-607-7

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Query Match          73.4%; Score 679; DB 2; Length 208;
Best Local Similarity 67.9%; Pred. No. 7.5e-65;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

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Db      22 IDLLYWRDIKQTGIVFGSFLLLFLSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 81

Qy      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLM 122
      |:|||||:| | | | | : : | : | : | : | : | : | : | : | : | : | : |
Db      82 KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLM 141

Qy      123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
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Qy      183 GLKRKAD 189
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Db      202 GAKRHAE 208

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RESULT 3

US-08-700-607-6

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; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Goli, Surya K.
;   APPLICANT: Hillman, Jennifer L.
;   TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: U.S.
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/700,607
;     FILING DATE: Filed Herewith
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0114 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 356 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     IMMEDIATE SOURCE:
;       LIBRARY: GenBank
;       CLONE: 307309
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US-08-700-607-6

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Query Match          73.4%;  Score 679;  DB 2;  Length 356;
Best Local Similarity 67.9%;  Pred. No. 1.6e-64;
Matches 127;  Conservative 31;  Mismatches 29;  Indels 0;  Gaps 0;
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Db      170 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 229

Qy      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLM 122
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Db      230 KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKLRLFLVQDLVDLSLKFAVLM 289
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;      MOLECULE TYPE:  peptide
;      IMMEDIATE SOURCE:
;      LIBRARY:      GenBank
;      CLONE:       281046
US-08-700-607-8

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Query Match 71.9%; Score 665; DB 2; Length 267;  
Best Local Similarity 67.2%; Pred. No. 3.3e-63;  
Matches 123; Conservative 32; Mismatches 28; Indels 0; Gaps 0;

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Qy	63	KSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLDVDSLKFVLM	122
Db	73	KTDEGHPPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKELRRLFLVQDLVDLSLKFVLM	132
Qy	123	WVF TYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA KIP	182
Db	133	WLLTYVGALENGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQA KIP	192
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## RESULT 6

US-09-149-476-563

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; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,633  
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; EARLIER APPLICATION NUMBER: 60/047,583  
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Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;

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Qy      84 LVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMMWFYTVYGALFNGLTLLILALI 143
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; Sequence 3, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Goli, Surya K.
;   APPLICANT: Hillman, Jennifer L.
;   TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: U.S.
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/700,607
;     FILING DATE: Filed Herewith
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0114 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 241 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: THP1NOB01
; CLONE: 31870
US-08-700-607-3
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Query Match          55.8%; Score 516; DB 2; Length 241;
Best Local Similarity 59.9%; Pred. No. 2.6e-47;
Matches 94; Conservative 33; Mismatches 30; Indels 0; Gaps 0;
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Qy      1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
      :| ||: |||: ||| ||| :| :||| ||::|| :|: ||||| ||||| ||||
Db      47 AVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLIALALLSVTISFRIYKSVIIQA 106

Qy      61 IQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
      :|||: ||||: |||: :: :| | | |:|: |:| :| : ||||: ||||| ||
Db      107 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 166

Qy      121 LMWVFYVVGALFNGLTLLILALISLFSIPVIYERHQV 157
      ||: ||||: |||: ||||| : : |:|::| ::|
Db      167 FMWLMTYVGAVFNGITLLILAEELLIXSVPIVYXKYKV 203
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# RESULT 8

US-09-149-476-411

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; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11

; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599

; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,881  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,908  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,669  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/049,610  
; EARLIER FILING DATE: 1997-06-13  
; EARLIER APPLICATION NUMBER: 60/061,060  
; EARLIER FILING DATE: 1997-10-02

Query Match

30.9%; Score 286; DB 4; Length 92;

Best Local Similarity 56.0%; Pred. No. 2.9e-23;  
Matches 51; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 90 NSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIP 149  
|::| |::| :| : |||||:|||||| || ||: |||||:||||:|||||| : :||:|  
Db 2 NAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAEELLIFSVP 61  
  
Qy 150 VIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
::||::: |||||:|:| | : || :|  
Db 62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92

RESULT 9

US-08-905-223-411

; Sequence 411, Application US/08905223

; Patent No. 6222029

; GENERAL INFORMATION:

; APPLICANT: Edwards, Jean-Baptiste D.

; APPLICANT: Duelert, Aymeric

; APPLICANT: Lacroix, Bruno

; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS

; NUMBER OF SEQUENCES: 503

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 501 West Broadway

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-3505

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Win95

; SOFTWARE: Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/905,223

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Israelsen, Ned A.

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 235-8550

; TELEFAX: (619) 235-0176

; INFORMATION FOR SEQ ID NO: 411:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

; ORIGINAL SOURCE:

; ORGANISM: Homo Sapiens

; TISSUE TYPE: Brain

; FEATURE:

; NAME/KEY: sig\_peptide

; LOCATION: -78..-1

; IDENTIFICATION METHOD: Von Heijne matrix  
; OTHER INFORMATION: score 6.3  
; OTHER INFORMATION: seq TLIMLLSWQLSVS/SV  
US-08-905-223-411

Query Match 10.8%; Score 100; DB 3; Length 80;  
Best Local Similarity 57.1%; Pred. No. 0.002;  
Matches 20; Conservative 8; Mismatches 5; Indels 2; Gaps 1;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLS--ITVFSI 33  
:| ||::|||:|||| ||| :| :||| |:| |:  
Db 46 AVHDLIFWRDVKKTGFVFGTTLIMLLSWQLSVSSV 80

RESULT 10

US-08-487-596-8

; Sequence 8, Application US/08487596  
; Patent No. 6440681

; GENERAL INFORMATION:

; APPLICANT: Elliot, Kathryn J.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Harpold, Michael M.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND  
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL  
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,596  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO US94/02447  
; FILING DATE: 08-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/149,503  
; FILING DATE: 08-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/028,031  
; FILING DATE: 08-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/938,154  
; FILING DATE: 30-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/504,455  
; FILING DATE: 03-APR-1990

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Seidman, Stephanie L.
;   REGISTRATION NUMBER: 33,779
;   REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619-238-0999
;   TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 468 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-487-596-8

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Query Match          10.3%; Score 95; DB 4; Length 468;
Best Local Similarity 21.5%; Pred. No. 0.078;
Matches 41; Conservative 33; Mismatches 61; Indels 56; Gaps 7;

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Qy      24 LLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHP- 69
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Db      288 VLVSLTVFLLVIEEIIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRSSSTHNA 347

Qy      70 -----FRAYLESEVAISEELVQ----KYSNSALGHVNSTIKELRRLF 107
      |:::  ||          | | : |   ::|: : |
Db      348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy      108 L----VDDLVDLSLKf-----AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 157
      :   | ::|: ||          : :| | :|          |: : || :|||: :
Db      408 MKENDVREVVEDWKFI AQVLD RMFLWTF LFVS-----IVGSLGLF-VPVIYKWANI 457

Qy      158 QIDHYLGLANK 168
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Db      458 LIPVHIGNANK 468

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# RESULT 11

US-08-660-451A-8

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; Sequence 8, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
;   APPLICANT: Elliott, Kathryn J.
;   APPLICANT: Harpold, Michael M.
;   TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
;   TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
;   NUMBER OF SEQUENCES: 20
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Brown, Martin, Haller & McClain
;     STREET: 1660 Union Street
;     CITY: San Diego
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 92101-2926
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS

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; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-660-451A-8

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Query Match          10.3%; Score 95; DB 4; Length 468;
Best Local Similarity 21.5%; Pred. No. 0.078;
Matches 41; Conservative 33; Mismatches 61; Indels 56; Gaps 7;

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Qy      24 LLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVIAIQKSDEGHP- 69
      :|:||||| :|          : |:  :: ||:| :  |  :|  |
Db      288 VLVSLTVFLLVIEEIIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRSSSTHNA 347

Qy      70 -----FRAYLESEVAISEELVQ----KYSNSALGHVNSTIKELRRLF 107
      |:::  ||  | | : |  ::|: : |
Db      348 MAPLVRKIFLHTLPKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy      108 L----VDDLVDLKF-----AVLMWVFVTVGALFENGLTLLILALISLFSIPVIYERHQV 157
      :  | ::|: ||  : :| | :|  | :  || :|||:  :
Db      408 MKENDVREVVEDWKFIAQVLDRLMFLWTFLEVS-----IVGSLGLF-VPVIYKWANI 457

Qy      158 QIDHYLGLANK 168
      |  ::| |||
Db      458 LIPVHIGNANK 468

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# RESULT 12

US-09-462-136-2

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; Sequence 2, Application US/09462136
; Patent No. 6426198
; GENERAL INFORMATION:
; APPLICANT: Carstea, et al.
; TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease

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; FILE REFERENCE: 4239-53894
; CURRENT APPLICATION NUMBER: US/09/462,136
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: PCT/US98/13862
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/051,682
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-136-2
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Query Match          9.6%; Score 88.5; DB 4; Length 1278;
Best Local Similarity 25.7%; Pred. No. 1.6;
Matches 39; Conservative 25; Mismatches 51; Indels 37; Gaps 7;
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Qy      46 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 105
      ::|||  : :  : :  : |      | ||  :: | : |||  || ||
Db      598 NLTISFTAERSIEDELNRESDSDF-----TVVISYAIMFLYISIALGH----IKSCRR 647

Qy      106 LFLVDD-----LVDSLKFAVLMWVFTYVGALENGLTLLILALI-----SLF 146
      | |||  :  :  | : ||:|  |||::: |  :|
Db      648 L-LVDSKVSLGIAGILIVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703

Qy      147 SIPVIYERHQ----VQIDHYLGLANKSVKDAM 174
      :  |:| :  :|  ||  | :|
Db      704 ILVQAYQORDERLQGETLDQQQLGRVLGEVAPSM 735
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# RESULT 13

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US-09-134-000C-5477
; Sequence 5477, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5477
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5477
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Query Match          9.4%; Score 86.5; DB 4; Length 592;
Best Local Similarity 20.9%; Pred. No. 0.88;
Matches 49; Conservative 41; Mismatches 61; Indels 83; Gaps 12;
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TELEPHONE: (240) 314-1224

```

;           TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 5246:
;           SEQUENCE CHARACTERISTICS:
;               LENGTH: 414 amino acids
;               TYPE: amino acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;           MOLECULE TYPE: protein
;           SEQUENCE DESCRIPTION: SEQ ID NO: 5246:
US-08-956-171E-5246

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Query Match          9.3%;   Score 86;   DB 4;   Length 414;
Best Local Similarity 22.2%;   Pred. No. 0.61;
Matches   42;   Conservative   37;   Mismatches   78;   Indels   32;   Gaps   7;

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```

Qy      2 VVDLLYWRDIKKTGV-VFGASLFLLLSLTVFSIVSVTAYI-ALALLSVTISFRIYKGV IQ 59
      :| ||: |:|: | : :   | ||::|   : |: | | |:| | |: |
Db      3 IVILLELRNIRTTAISIIISIPLSLLMALIALKLSVDVSLNILTGLALTVAIG-RVIDDSIV 61

Qy      60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRRLFLVDDLVDLSLKFA 119
      ::   : :| :|| : | :   : | |: : : || : |
Db      62 VVE-----NIYRRLTDSEEQLKGENL-----IISATTEVFVKPIMSSTLVTTIIVFL 106

Qy      120 VLMWVFETYVGALEN-----GLTLLILALISLFSIPVI-----YERHQVQIDHYLGL 165
      |:| ||:| :|| |:| :| :   :| | | ||:
Db      107 PLVFSVSGSVGEMFRPFALAIAFSLLASLLVSITLVPALAAATLFKKGVKRRNKQHQEGLGV 166

Qy      166 ANKSVKDAM 174
      : : | :
Db      167 VSTTYKKVL 175

```

# RESULT 15

```

US-09-134-001C-5005
; Sequence 5005, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5005
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5005

```

```

Query Match          9.2%;   Score 85.5;   DB 4;   Length 1051;
Best Local Similarity 22.1%;   Pred. No. 2.5;

```

Matches 43; Conservative 39; Mismatches 62; Indels 51; Gaps 9;

```
Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSV-----TAYIALALLSVTISFRIYKG 56
      :| ||: |:|: | :                |||:  | || | :|:::
Db      380 IVILLEFLRNIRTTAI-----SIVSIPMSILIALIALKLSNVSLNITLGA 424

Qy      57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYS--NSALGHVNSTIKELRRLF---LVDD 111
      : || :                :: : : | : :: | | | | | :| :
Db      425 LTVAIGR-----VIDDSIVVVENIFRRLSDPNEKLGKGENLIISATREVFKEPIMSST 475

Qy     112 LVDSLKFAVLMWVFTYVGALEN----GLTLLILA--LISLFSIPVI---YERHQVQIDHY 162
      || : | |::|  || :|      :| :|| |:: :| :  : ::
Db      476 LVTIVVFLPLVVFVSGSVGEMFRPFALAITFSLLASLLVSITLVPSLGATFFKN----- 528

Qy     163 LGLANKSVKDAMAKI 177
      |: |: |: : :
Db      529 -GVKNREQKEGLGTV 542
```

Search completed: September 29, 2004, 18:21:00  
Job time : 6.69196 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:05:43 ; Search time 4.62587 Seconds  
(without alignments)  
3930.111 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	679	73.4	208	2	I60904	neuroendocrine-spe
2	679	73.4	776	2	A46583	neuroendocrine-spe
3	665	71.9	267	2	A60021	tropomyosin-relate
4	321	34.7	2484	2	T26216	hypothetical prote
5	321	34.7	2607	2	T26215	hypothetical prote
6	320	34.6	222	2	T26213	hypothetical prote
7	194	21.0	255	2	E84899	hypothetical prote
8	182	19.7	271	2	T13013	hypothetical prote
9	163	17.6	275	2	T05595	hypothetical prote
10	142	15.4	393	2	S67763	probable membrane
11	135.5	14.6	242	2	B85016	hypothetical prote
12	134	14.5	183	2	A84527	hypothetical prote
13	131.5	14.2	295	2	S59439	probable membrane

14	123	13.3	206	2	T01153	probable seed matu
15	109.5	11.8	264	2	T47948	hypothetical prote
16	107.5	11.6	203	2	T47571	hypothetical prote
17	94	10.2	288	2	B90043	conserved hypothet
18	93.5	10.1	457	2	H85095	hypothetical prote
19	92.5	10.0	458	2	A72258	hypothetical prote
20	92.5	10.0	677	2	F95232	immunity protein,
21	92.5	10.0	680	2	H98096	conserved hypothet
22	91	9.8	160	2	C84422	hypothetical prote
23	90.5	9.8	442	2	C75057	hypothetical prote
24	89	9.6	224	2	D71915	hydrogenase, cytoc
25	89	9.6	468	2	A38223	nicotinic acetylch
26	87	9.4	1065	2	E69795	acriflavin resista
27	86	9.3	589	2	F64201	transport ATP-bind
28	86	9.3	1055	2	H90023	hypothetical prote
29	85.5	9.2	296	2	S46018	probable membrane
30	85.5	9.2	299	2	B69155	hypothetical prote
31	85	9.2	299	2	C64397	hypothetical prote
32	85	9.2	459	2	G86264	F3F19 hypothetical
33	85	9.2	689	2	T09007	ABC-transporter ho
34	84.5	9.1	151	2	G96705	unknown protein, 7
35	83.5	9.0	445	2	AD2358	glucosyltransferas
36	83.5	9.0	570	2	S52765	secD protein - Str
37	83.5	9.0	823	2	H83724	hypothetical prote
38	83	9.0	180	2	E97200	probable phosphata
39	83	9.0	252	2	G97886	hypothetical prote
40	83	9.0	388	1	D70006	conserved hypothet
41	82.5	8.9	410	2	A95044	conserved hypothet
42	82.5	8.9	502	2	F70316	conserved hypothet
43	82.5	8.9	675	2	T50332	SCT1 homolog SPBC1
44	82.5	8.9	937	2	T41400	probable peroxisom
45	82	8.9	224	1	A64599	hydrogenase (EC 1.

#### ALIGNMENTS

##### RESULT 1

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

```
Query Match          73.4%;  Score 679;  DB 2;  Length 208;
Best Local Similarity 67.9%;  Pred. No. 2.5e-52;
Matches 127;  Conservative 31;  Mismatches 29;  Indels 0;  Gaps 0;

Qy      3  VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62
      :|||||||:|:|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     22  IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 81

Qy     63  KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVIM 122
      |:|||||:| | | | | : : | | : | | : : : | | | | | | | | | | | | | | |
Db     82  KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVIM 141

Qy    123  WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
      |: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    142  WLLTYVGALFNGLTLLLMAVVSMTLPVVYVKHQQIDQYLGLVRTHINAVVAKIQAKIP 201

Qy    183  GLKRKAD 189
      | | | |
Db    202  GAKRHAE 208
```

#### RESULT 2

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 421-776 <ROE2>

A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

```
Query Match          73.4%;  Score 679;  DB 2;  Length 776;
Best Local Similarity 67.9%;  Pred. No. 1.2e-51;
Matches 127;  Conservative 31;  Mismatches 29;  Indels 0;  Gaps 0;
```

## T26216



hypothetical protein W06A7.3c - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T26216

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26216

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2484 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3c

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 34.7%; Score 321; DB 2; Length 2484;

Best Local Similarity 32.6%; Pred. No. 1.1e-19;

Matches 60; Conservative 46; Mismatches 78; Indels 0; Gaps 0;

```
Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
      |:|::| | | | | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      2289 VLDVIYWRDAKKS AIVLSLALLVLFVLAKYPLLT VVTYSLLLALGAAAGFRVFKKVEAQI 2348

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121
      :|:| | | | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      2349 KKT DSEHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFGGLV 2408

Qy      122 MWVFTYVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
      :| | | :| :| | | | :| :| :| :| :| :| :| :| :| :| :| :|
Db      2409 LWSLTYIASWFSGFTLAILGLLGVSVPK VYESNQEAIDPHLATISGHLKNVQNIIDEKL 2468

Qy      182 PGLK 185
      | | :
Db      2469 PFLR 2472
```

RESULT 5

T26215

hypothetical protein W06A7.3a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T26215

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2607 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3a

A;Map position: 5

Qy	2	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI	61
		::::      : :  :  :    : ::          : ::	
Db	27	ILDVIYWDRDAKKSAIVLSLALLLVLFVLAKYPLLTWVTYSLLLALGAAAGFRVFVKVEAQI	86
Qy	62	QKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLDVDSLKFAVL	121
		: :        :: : :    :: :   : ::   : : :: :  ::	
Db	87	KKTDSEHPFSEILAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFGGLV	146
Qy	122	MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLG LANKSVKDAMAKIQAKI	181

```

      :| ||: : |:| || || |: :||:| :|| :| || :| : :|: | |:
Db      147 LWSLTYIASWFSGFTLAILGLLGVSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL 206

Qy      182 PGLK 185
      | |:
Db      207 PFLR 210

```

RESULT 7

E84899

hypothetical protein At2g46170 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C;Accession: E84899

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;  
 Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,  
 C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,  
 L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,  
 M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhagen,  
 G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,  
 C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84899

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-255 <STO>

A;Cross-references: GB:AE002093; NID:g3702332; PIDN:AAC62889.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g46170

A;Map position: 2

```

Query Match          21.0%; Score 194; DB 2; Length 255;
Best Local Similarity 27.6%; Pred. No. 1.1e-09;
Matches 54; Conservative 41; Mismatches 77; Indels 24; Gaps 6;

```

```

Qy      4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
      |: ||| |:| | | :||:| | :||: |:|: | :|
Db      70 DVFLWRDKKLSGAVLGVATAIWVLFELVEYHLLSLLCHISILALG---GLFLWSNAHTLI 126

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121
      |: | :| :| | :|| :|| :| :| :| | | | |
Db      127 NKTSPQIP-----EIHVP EEAFLLV VASSLRNELNQAFVILRSIALGRDLKKFLMVVVG 179

Qy      122 MWVFTYVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM----- 174
      |: : || || ||: : : | :||: ||: |:| :| || |:|:
Db      180 LWIISVVGNNWFNFLTIVYICFVILHTVPMLYEKHEDKVD---PLAEKAMKELQKQYVVF 236

Qy      175 AKIQAKIP--GLKRKA 188
      |: :||| || ||
Db      237 EKVLSKIPIASLKAKA 252

```

RESULT 8

T13013

hypothetical protein F8L21.10 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 22-Oct-1999  
 C;Accession: T13013  
 R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.  
 submitted to the Protein Sequence Database, July 1999  
 A;Reference number: Z17587  
 A;Accession: T13013  
 A;Molecule type: DNA  
 A;Residues: 1-271 <BEV>  
 A;Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.10  
 A;Experimental source: cultivar Columbia; BAC clone F8L21  
 C;Genetics:  
 A;Gene: ATSP:F8L21.10  
 A;Map position: 4  
 A;Introns: 85/1; 145/2; 192/3; 216/1

Query Match 19.7%; Score 182; DB 2; Length 271;  
 Best Local Similarity 25.6%; Pred. No. 1.4e-08;  
 Matches 46; Conservative 43; Mismatches 79; Indels 12; Gaps 3;

```

Qy      4 D L L Y W R D I K K T G V V F G A S -- L F L L L S L T V F S I V S V T A Y I A L A L L S V T I S F R I Y K G V I Q A I 61
      | : | | : | | | : : | | : : : : : : | : | : : |
Db      87 D I F M W K D K K M S G G V F G G A T V A W V L F E L M E Y H L L T L L C H V M I V A L A V L F --- L W S N A T M F I 143

Qy      62 Q K S D E G H P F R A Y L E S E V A I S E E L V Q K Y S N S A L G H V N S T I K E L R R L F L V D D L V D S L K F A V L 121
      || | | | | | | | | : : : : : : | | | | : | : |
Db      144 H K S P P K I P ----- E V H I P E E P L L Q L A S G L R I E I N R G I S S L R E I A S G R D I K K F L S A I A G 196

Qy      122 M W V F T Y V G A L F N G L T L L I L A L I S L F S I P V I Y E R H Q V Q I D H Y L G L A N K S V K D A M A K I Q A K I 181
      : | | : : | : : | | | : | | : | | : : : : : | | | : | | : | | :
Db      197 L W V L S I L G G C Y S F L T L A Y I A L V L L F T V P L F Y D K Y E D K V D S Y G E K A M A E L K K Q Y A V L D A K V 256
  
```

# RESULT 9

T05595

hypothetical protein F9D16.100 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 23-Jul-1999  
 C;Accession: T05595  
 R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.;  
 Mayer, K.F.X.; Schueller, C.  
 submitted to the Protein Sequence Database, February 1999  
 A;Reference number: Z15419  
 A;Accession: T05595  
 A;Molecule type: DNA  
 A;Residues: 1-275 <BEV>  
 A;Cross-references: EMBL:AL035394  
 A;Experimental source: cultivar Columbia; BAC clone F9D16  
 C;Genetics:  
 A;Map position: 4  
 A;Introns: 89/1; 149/2; 196/3; 220/1  
 A;Note: F9D16.100

Query Match 17.6%; Score 163; DB 2; Length 275;  
 Best Local Similarity 25.5%; Pred. No. 6.4e-07;

Matches 49; Conservative 43; Mismatches 82; Indels 18; Gaps 5;

```

Qy      4 D L L Y W R D I K K T G V V F G -- A S L F L L L S L T V F S I V S V T A Y I A L A L L S V T I S F R I Y K G V I Q A I 61
      | : | : | : | | : : : | : : : : : : : : | : |
Db      91 D I F M W K N K K M S G G V L G G A T A A W V F E L M E Y H L L T L L C H V M I V V L A V L F --- L W S N A T M F I 147

Qy      62 Q K S D E G H P F R A Y L E S E V A I S E E L V Q K Y S N S A L G H V N S T I K E L R R L F L V D D L V D S L K F A V L 121
      | | | | | | | | | | | | | : : : : : | : | : | |
Db      148 N K S P P K I P ----- E V H I P E E P I L Q L A S G L R I E I N R G F S S L R E I A S G R D L K K F L I A I A G 200

Qy      122 M W V F T Y V G A L F N G L T L L I L A L I S L F S I P V I Y E R H Q V Q I D H Y L G L A N K S V K D A M A --- K I 177
      : | | : : | | | | | : | : | : | : : : : : | : | : | :
Db      201 L W V L S I L G G C F N F L T L A Y I A L V L L F T V P L A Y D K Y E D K V D P L G E K A M I E L K K Q Y A V L D E K V 260

Qy      178 Q A K I P -- G L K R K 187
      : | | | | |
Db      261 L S K I P L G P L K N K 272

```

# RESULT 10

S67763

probable membrane protein YDL204w - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein D1062

C;Species: *Saccharomyces cerevisiae*

C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 19-Apr-2002

C;Accession: S67763

R;Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67756

A;Accession: S67763

A;Molecule type: DNA

A;Residues: 1-393 <SCH>

A;Cross-references: EMBL:Z74252; NID:g1431337; PID:e253109; PID:g1431338;

GSPDB:GN00004; MIPS:YDL204w

A;Experimental source: strain S288C

C;Genetics:

A;Gene: MIPS:YDL204w

A;Cross-references: SGD:S0002363

A;Map position: 4L

C;Keywords: transmembrane protein

F;50-66/Domain: transmembrane #status predicted <TM1>

F;150-166/Domain: transmembrane #status predicted <TM2>

Query Match 15.4%; Score 142; DB 2; Length 393;

Best Local Similarity 26.3%; Pred. No. 6.8e-05;

Matches 45; Conservative 34; Mismatches 56; Indels 36; Gaps 4;

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Qy      5 L L Y W R D I K K T G V V F G A S L F L L L S L T V F S I V S V T A Y I A L A L L S V T I S F R I Y K G V I Q A I Q K S 64
      | : | | : | : | | | : : : | | : | :
Db      33 L I Y W T N P S K S G A S F A A T L V S L L I L R N V N V I S V L L K I G Y M V L F T S ----- 76

Qy      65 D E G H P F R A Y L E S E V A I S E E L V Q K Y ---- S N S A L G H V N S T I - K E L R R L F L V D D L V D S L K F A 119
      | | : | : : | : | : | : | | : | : | |
Db      77 ----- F A V E L S T K V L F D K G V V S R F G M Q E S P D L V G V L K P H I D R E L D R L P A E L D R I R K L V F A 131

Qy      120 ----- V L M W V F T Y V G A L F N G L T L L I L A L I S L F S I P V I Y E R H Q V Q I D 160
      | : : : | : : | : | : | : | : | : |

```



G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.  
 Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A;Reference number: A84420; MUID:20083487; PMID:10617197  
 A;Accession: A84527  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-183 <STO>  
 A;Cross-references: GB:AE002093; NID:g4662633; PIDN:AAD26905.1; GSPDB:GN00139  
 C;Genetics:  
 A;Gene: At2g15280  
 A;Map position: 2

Query Match 14.5%; Score 134; DB 2; Length 183;  
 Best Local Similarity 24.6%; Pred. No. 0.00014;  
 Matches 44; Conservative 38; Mismatches 79; Indels 18; Gaps 4;

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Qy      8 WRDIKKTGVVFGAS-----LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62
      |:: :  :: |::  || : | | : ||| | | | |
Db      2 WKNRRGGFLLLGSTLLWFLFEKCGYSFFPFV-----VNTQLLSVVILFLWAKSAI---- 52

Qy     63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLM 122
      : |  ||  |::| |  ::  :|: : |:: :  :|::
Db     53 LFNRPMPQLPNLE----ITEEFVFMVADAIRVWINTVLAVAREIYVGRNAKQLFRVSVVL 108

Qy    123 WVFYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
      | ::||  | ||:| | ::  || :|||:|  ||  | | :: ::  || ::
Db    109 WTVSFVGNFLNFLTILYLGVVLSLLIPFLYERYQDLIDEKLSLTHRVIQTQYRKIDERL 167
  
```

# RESULT 13

S59439

probable membrane protein YDR233c - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein YD9934.17c

C;Species: *Saccharomyces cerevisiae*

C;Date: 30-Nov-1995 #sequence\_revision 16-Feb-1996 #text\_change 19-Apr-2002

C;Accession: S59439

R;Murphy, L.; Harris, D.

submitted to the EMBL Data Library, March 1995

A;Reference number: S59423

A;Accession: S59439

A;Molecule type: DNA

A;Residues: 1-295 <MUR>

A;Cross-references: EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004;

MIPS:YDR233c

A;Experimental source: strain AB972

C;Genetics:

A;Gene: MIPS:YDR233c

A;Cross-references: SGD:S0002641

A;Map position: 4R

C;Keywords: transmembrane protein

F;40-56/Domain: transmembrane #status predicted <TM1>

F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 14.2%; Score 131.5; DB 2; Length 295;

Best Local Similarity 21.6%; Pred. No. 0.0004;  
Matches 45; Conservative 43; Mismatches 69; Indels 51; Gaps 5;

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Qy      4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQK 63
      ||| ||: :|| || || || | :::: :| :| | | :| :
Db      22 DLLLWRNPVQTGKYFGGSLALLLILKKVNLITFFLKVAYTILEFTT-----GSIEFV-- 72

Qy      64 SDEGHPFRAYLESEVAISEELVQKY-----SNSALGHVNSTIKEL-----RRLFL 108
      |:: : : | : || : : : | : : | : | : | : | :
Db      73 -----SKLFLGQGLITKYGPKECPNIAGFIKPHIDEALKQLPVFQAHIRKTVF 120

Qy      109 VDDLVDLSLKFAVLMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQID----- 160
      : | || ::: : | : |:: :| | |::||| : : :||
Db      121 AQVPKHTEKTAVALFLLHKFFSWFSIWTIVFVADIFTFTLPVIYHSYKHEIDATVAQGVE 180

Qy      161 -----HYLGLANKSVKDAMAKIQAKI 181
      : :| : | : |::|:
Db      181 ISKQKTQEF SQMACEKTKPYLDKVESKL 208
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#### RESULT 14

T01153

probable seed maturation protein [imported] - *Arabidopsis thaliana*

N;Alternate names: hypothetical protein F27L4.17

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 16-Feb-2001

C;Accession: T01153; T02426; C84627

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;  
Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.;  
Venter, J.C.

submitted to the EMBL Data Library, June 1998

A;Description: *Arabidopsis thaliana* chromosome II BAC F26B6 genomic sequence.

A;Reference number: Z14198

A;Accession: T01153

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-206 <ROU>

A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242725

A;Experimental source: cultivar Columbia

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;  
Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.;  
Venter, J.C.

submitted to the EMBL Data Library, May 1998

A;Description: *Arabidopsis thaliana* chromosome II BAC F27L4 genomic sequence.

A;Reference number: Z14658

A;Accession: T02426

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-206 <RO2>

A;Cross-references: EMBL:AC004482; NID:g3152602; PIDN:AAC17096.1; PID:g3152617

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;  
Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,  
C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,  
L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,  
M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhagen,  
G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,  
C.M.; Venter, J.C.



Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84627

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-206 <STO>

A;Cross-references: GB:AE002093; NID:g3152617; PIDN:AAC17096.1; GSPDB:GN00139  
C;Genetics:

A;Gene: At2g23640; F26B6.29; F27L4.17

A;Map position: 2

A;Introns: 14/1; 76/2; 147/1

C;Superfamily: *Arabidopsis thaliana* hypothetical protein F27L4.17

Query Match 13.3%; Score 123; DB 2; Length 206;  
Best Local Similarity 20.9%; Pred. No. 0.0015;  
Matches 40; Conservative 48; Mismatches 85; Indels 18; Gaps 4;

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Qy      2 VVDLLYWRDIKK--TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQ 59
      | | : | | | : : : | : || | | : : : : | : | : | : : : :
Db      16 VEDIYLWRRKKLAFSTLLVSTSTWILLSFYGFTTITIVSWIGIAVVS MIF---LWGSLLR 72

Qy      60 AIQKSDEGHPFRAYLESEVA---ISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLDSL 116
      : | : | : : : | : | : : | : | : : : : | : : :
Db      73 LLSK-----VEPELSGLEVSEEFV VETVRSCRMLMEEMVRWMFRVGAESEWFVFA 122

Qy      117 KEAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAK 176
      : : | : : : | : | : | : : : | : : : | : | : | : |
Db      123 RTVLGFWILSRIGNLLDFHTCLFIGLVMGLTPVKLWEEYGDQIQKHLGSLKDKSKGAYNT 182

Qy      177 IQAKIPGLKRRK 187
      | | : | |
Db      183 THEKILEMKNK 193
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#### RESULT 15

T47948

hypothetical protein F2A19.160 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C;Accession: T47948

R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.

submitted to the Protein Sequence Database, January 2000

A;Reference number: Z24480

A;Accession: T47948

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-264 <DEH>

A;Cross-references: EMBL:AL132962

A;Experimental source: cultivar Columbia; BAC clone F2A19

C;Genetics:

A;Map position: 3

A;Introns: 68/1; 128/2; 164/1; 210/1

A;Note: F2A19.160

Query Match 11.8%; Score 109.5; DB 2; Length 264;  
 Best Local Similarity 24.9%; Pred. No. 0.03;  
 Matches 54; Conservative 38; Mismatches 68; Indels 57; Gaps 14;

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Qy      4 D L L Y W R D I K K T G V V F G -- A S L F L L L S L T V F S I V S V T A Y I ----- A L A L L S V T I S F R I Y K 55
      | : | | | | : | | : : : | | : : | : | | | | : | : |
Db      70 D V F L W R D K K L S A S V L G V A T A I W V L F E L V E Y H F L S I V C H I L I F A L A A L F L L S N A H A F - M N K 128

Qy      56 G V I Q ----- A I Q K S D E G ----- H P F R A Y L E S E V A I S E E L V Q K - Y S N - S A L G H V N S T I K E 102
      | : : : | | | | | | | | | | : | | | : | | |
Db      129 G T F P Y D C F C T E K R A E P G L C Y F K E H C L R K G L E E --- I S H E L I Q S T Y E T F S I M G F V T R T --- 182

Qy      103 L R R L F L V D D L V D S L K F A V L -- M W V F T Y V G A L F N G -- L T L L I L A L I S L F S I P V I Y E R H Q V Q 158
      | : : | : | : | | : | : | : | : | : | : |
Db      183 ----- S I Y I G I S G G F W A V D N L G C --- G K L V Q L L D S C F V L H T V P M L Y E K H E D K 227

Qy      159 I D H Y L G L A N K S V K D A M ----- A K I Q A K I P G L K R K A 188
      : | : | : | : | : | : | : | : |
Db      228 V D --- P V A E K T L K E L K K H Y M V F D E K V L S K L P V A S L K A 261

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Search completed: September 29, 2004, 18:15:52

Job time : 6.62587 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:16:15 ; Search time 20.2878 Seconds  
(without alignments)  
2997.869 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWRIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match Length	ID	Description
No.					

1	925	100.0	1163	9	US-09-893-348-18	Sequence 18, Appl
2	922	99.7	379	14	US-10-205-194-164	Sequence 164, App
3	921	99.6	199	9	US-09-893-348-21	Sequence 21, Appl
4	921	99.6	360	9	US-09-893-348-20	Sequence 20, Appl
5	908	98.2	1192	9	US-09-789-386-2	Sequence 2, Appli
6	908	98.2	1192	9	US-09-758-140-6	Sequence 6, Appli
7	908	98.2	1192	9	US-09-893-348-23	Sequence 23, Appl
8	908	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appli
9	908	98.2	1192	12	US-10-267-502-429	Sequence 429, App
10	908	98.2	1192	14	US-10-060-036-71	Sequence 71, Appl
11	908	98.2	1192	16	US-10-327-213-9	Sequence 9, Appli
12	908	98.2	1192	16	US-10-466-258-9	Sequence 9, Appli
13	906.5	98.0	1163	12	US-10-267-502-431	Sequence 431, App
14	904	97.7	199	9	US-09-893-348-25	Sequence 25, Appl
15	904	97.7	199	12	US-10-660-946-1	Sequence 1, Appli
16	904	97.7	373	9	US-09-789-386-6	Sequence 6, Appli
17	904	97.7	373	9	US-09-765-205-6	Sequence 6, Appli
18	904	97.7	373	9	US-09-893-348-24	Sequence 24, Appl
19	904	97.7	373	12	US-10-408-967-8	Sequence 8, Appli
20	904	97.7	373	14	US-10-060-036-72	Sequence 72, Appl
21	904	97.7	373	16	US-10-466-258-4	Sequence 4, Appli
22	901	97.4	1192	12	US-10-408-967-7	Sequence 7, Appli
23	897	97.0	199	12	US-10-408-967-9	Sequence 9, Appli
24	895	96.8	199	12	US-09-978-360A-467	Sequence 467, App
25	864	93.4	199	16	US-10-466-258-11	Sequence 11, Appl
26	679	73.4	208	12	US-10-660-946-7	Sequence 7, Appli
27	679	73.4	356	12	US-10-660-946-6	Sequence 6, Appli
28	679	73.4	776	12	US-10-660-946-5	Sequence 5, Appli
29	679	73.4	776	12	US-10-267-502-430	Sequence 430, App
30	678	73.3	777	14	US-10-205-219-93	Sequence 93, Appl
31	678	73.3	780	12	US-10-267-502-432	Sequence 432, App
32	665	71.9	267	12	US-10-660-946-8	Sequence 8, Appli
33	665	71.9	267	14	US-10-205-194-127	Sequence 127, App
34	622.5	67.3	236	9	US-09-729-674-20	Sequence 20, Appl
35	622.5	67.3	236	9	US-09-765-205-26	Sequence 26, Appl
36	622.5	67.3	236	12	US-10-408-967-2	Sequence 2, Appli
37	622.5	67.3	266	12	US-10-276-774-2330	Sequence 2330, Ap
38	622.5	67.3	269	14	US-10-106-698-6222	Sequence 6222, Ap
39	617.5	66.8	593	15	US-10-108-260A-2892	Sequence 2892, Ap
40	539.5	58.3	168	10	US-09-809-391-563	Sequence 563, App
41	539.5	58.3	168	10	US-09-882-171-563	Sequence 563, App
42	539.5	58.3	168	12	US-10-164-861-563	Sequence 563, App
43	520	56.2	222	12	US-10-267-502-428	Sequence 428, App
44	516	55.8	241	12	US-10-660-946-3	Sequence 3, Appli
45	507.5	54.9	234	12	US-10-424-599-200840	Sequence 200840,

#### ALIGNMENTS

RESULT 1  
 US-09-893-348-18  
 ; Sequence 18, Application US/09893348  
 ; Patent No. US20020072493A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal

```

; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

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Query Match          100.0%; Score 925; DB 9; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60
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Db      975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1034
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Qy      61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120
          |||
Db      1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1094
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Qy      121 LMWVFTYVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
          |||
Db      1095 LMWVFTYVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
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Qy      181 IPGLKRKAD 189
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Db      1155 IPGLKRKAD 1163

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# RESULT 2

US-10-205-194-164

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; Sequence 164, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

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; FILE REFERENCE: WL-A-018201  
 ; CURRENT APPLICATION NUMBER: US/10/205,194  
 ; CURRENT FILING DATE: 5200-07-24  
 ; PRIOR APPLICATION NUMBER: GB 0118354.0  
 ; PRIOR FILING DATE: 2001-07-27  
 ; NUMBER OF SEQ ID NOS: 177  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 164  
 ; LENGTH: 379  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 ; FEATURE:  
 ; OTHER INFORMATION: Foocen-m2 reticulon  
 US-10-205-194-164

Query Match 99.7%; Score 922; DB 14; Length 379;  
 Best Local Similarity 99.5%; Pred. No. 4.6e-85;  
 Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 191 AVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 250  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 251 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 310  
 Qy 121 LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 311 LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 370  
 Qy 181 IPGLKRRKAD 189  
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 Db 371 IPGLKRRKAD 379

# RESULT 3

US-09-893-348-21

; Sequence 21, Application US/09893348  
 ; Patent No. US20020072493A1  
 ; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal  
 ; APPLICANT: COHEN, Irun R.  
 ; APPLICANT: BESERMAN, Pierre  
 ; APPLICANT: MOSONEGO, Alon  
 ; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A  
 ; CURRENT APPLICATION NUMBER: US/09/893,348  
 ; CURRENT FILING DATE: 2001-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/314,161  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: US 09/218,277  
 ; PRIOR FILING DATE: 1998-12-22  
 ; PRIOR APPLICATION NUMBER: PCT/US98/14715  
 ; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500  
 ; PRIOR FILING DATE: 1998-05-19  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 21  
 ; LENGTH: 199  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-09-893-348-21

Query Match 99.6%; Score 921; DB 9; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-85;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI	61
Db	12	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI	71
Qy	62	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLDFSLKFAVL	121
Db	72	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLDFSLKFAVL	131
Qy	122	MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	181
Db	132	MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	191
Qy	182	PGLKRRKAD	189
Db	192	PGLKRRKAD	199

RESULT 4

US-09-893-348-20

; Sequence 20, Application US/09893348  
 ; Patent No. US20020072493A1  
 ; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal  
 ; APPLICANT: COHEN, Irun R.  
 ; APPLICANT: BESERMAN, Pierre  
 ; APPLICANT: MOSONEGO, Alon  
 ; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A  
 ; CURRENT APPLICATION NUMBER: US/09/893,348  
 ; CURRENT FILING DATE: 2001-06-28  
 ; PRIOR APPLICATION NUMBER: US 09/314,161  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: US 09/218,277  
 ; PRIOR FILING DATE: 1998-12-22  
 ; PRIOR APPLICATION NUMBER: PCT/US98/14715  
 ; PRIOR FILING DATE: 1998-07-21  
 ; PRIOR APPLICATION NUMBER: IL 124500  
 ; PRIOR FILING DATE: 1998-05-19  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 20

; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-893-348-20

Query Match 99.6%; Score 921; DB 9; Length 360;  
Best Local Similarity 100.0%; Pred. No. 5.5e-85;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
          |||
Db      173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 232

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKLFAVL 121
          |||
Db      233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKLFAVL 292

Qy      122 MWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
          |||
Db      293 MWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352

Qy      182 PGLKRRKAD 189
          |||
Db      353 PGLKRRKAD 360
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RESULT 5

US-09-789-386-2

; Sequence 2, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-2

Query Match 98.2%; Score 908; DB 9; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 5.5e-83;  
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIA 60
          |||
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Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1063

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 |||

Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 |||

Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAD 189  
 |||

Db 1184 IPGLKRKAE 1192

RESULT 6

US-09-758-140-6

; Sequence 6, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth

; FILE REFERENCE: 44574-5073-US

; CURRENT APPLICATION NUMBER: US/09/758,140

; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: US 60/175,707

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: US 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,378

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-758-140-6

Query Match 98.2%; Score 908; DB 9; Length 1192;

Best Local Similarity 97.4%; Pred. No. 5.5e-83;

Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60  
 |||

Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1063

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 |||

Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 |||

Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAD 189

|||||||:  
Db 1184 IPGLKRKAE 1192

RESULT 7

US-09-893-348-23

; Sequence 23, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 23

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-893-348-23

Query Match 98.2%; Score 908; DB 9; Length 1192;

Best Local Similarity 97.4%; Pred. No. 5.5e-83;

Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60

|||||||:

Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120

|||||||:

Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123

Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180

|||||||:|||||||:

Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy 181 IPGLKRKAD 189

|||||||:

Db 1184 IPGLKRKAE 1192

RESULT 8

US-09-972-599A-6  
 ; Sequence 6, Application US/09972599A  
 ; Patent No. US20020077295A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STRITTMATTER, STEPHEN M.  
 ; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
 ; FILE REFERENCE: C077 CIP US  
 ; CURRENT APPLICATION NUMBER: US/09/972,599A  
 ; CURRENT FILING DATE: 2001-10-06  
 ; PRIOR APPLICATION NUMBER: PCT/US01/01041  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 09/758,140  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: 60/236,378  
 ; PRIOR FILING DATE: 2000-09-29  
 ; PRIOR APPLICATION NUMBER: 60/207,366  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/175,707  
 ; PRIOR FILING DATE: 2000-01-12  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-972-599A-6

Query Match 98.2%; Score 908; DB 9; Length 1192;  
 Best Local Similarity 97.4%; Pred. No. 5.5e-83;  
 Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
 |||  
 Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 |||  
 Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAV 1123  
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 |||:|||||:|||||:|||||  
 Db 1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183  
 Qy 181 IPGLKRKAD 189  
 |||||:  
 Db 1184 IPGLKRKAE 1192

RESULT 9  
 US-10-267-502-429  
 ; Sequence 429, Application US/10267502  
 ; Publication No. US20040071700A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kim, Jaeseob  
 ; APPLICANT: Galant, Ron  
 ; TITLE OF INVENTION: Obesity Linked Genes  
 ; FILE REFERENCE: LSD-07416

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; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-429
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Query Match 98.2%; Score 908; DB 12; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 5.5e-83;  
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	1	SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV	60
Db	1004	SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV	1063
Qy	61	IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD	120
Db	1064	IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD	1123
Qy	121	LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA	180
		:     :	
Db	1124	LMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA	1183
Qy	181	IPGLKRKAD	189
		:	
Db	1184	IPGLKRKAE	1192

RESULT 10

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 71

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-060-036-71

Query Match 98.2%; Score 908; DB 14; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 5.5e-83;

Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy      1  SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1063

Qy      61  IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLVLKFAV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVLKFAV 1123

Qy      121  LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
          ||||||||||||||||||||||||:||||||| |||||||||:|||||||
Db      1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy      181  IPGLKRKAD 189
          |||||||:
Db      1184 IPGLKRKAE 1192
```

RESULT 11

US-10-327-213-9

; Sequence 9, Application US/10327213

; Publication No. US20040121341A1

; GENERAL INFORMATION:

; APPLICANT: FILBIN, MARIE T.

; APPLICANT: DOMENICONI, MARCO

; APPLICANT: CAO, ZIXUAN

; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)

; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION

; FILE REFERENCE: CUNY/003

; CURRENT APPLICATION NUMBER: US/10/327,213

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-327-213-9

Query Match 98.2%; Score 908; DB 16; Length 1192;

Best Local Similarity 97.4%; Pred. No. 5.5e-83;

Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy      1  SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1063

Qy      61  IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLVLKFAV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVLKFAV 1123

Qy      121  LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
          ||||||||||||||||||||||||:||||||| |||||||||:|||||||
Db      1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy      181  IPGLKRKAD 189
```

|||||||:  
Db 1184 IPGLKRKAE 1192

RESULT 12

US-10-466-258-9

; Sequence 9, Application US/10466258  
; Publication No. US20040132096A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: ASSAY  
; FILE REFERENCE: P80966 GCW  
; CURRENT APPLICATION NUMBER: US/10/466,258  
; CURRENT FILING DATE: 2003-07-15  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-466-258-9

Query Match 98.2%; Score 908; DB 16; Length 1192;  
Best Local Similarity 97.4%; Pred. No. 5.5e-83;  
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
|||||||  
Db 1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1063  
QY 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKFV 120  
|||||||  
Db 1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFV 1123  
QY 121 LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
|||||||:|||||||:|||||||  
Db 1124 LMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183  
QY 181 IPGLKRKAD 189  
|||||||:  
Db 1184 IPGLKRKAE 1192

RESULT 13

US-10-267-502-431

; Sequence 431, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 431

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;   LENGTH: 1163
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-267-502-431
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Qy	1	SVVDLLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ	59
Db	974	SVVDLLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ	1033
Qy	60	AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFA	119
Db	1034	AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFA	1093
Qy	120	VLMWVFETYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA	179
Db	1094	VLMWVFETYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA	1153
Qy	180	KIPGLKRRKAD	189
		:	
Db	1154	KIPGLKRRKAE	1163

Query Match 97.7%; Score 904; DB 9; Length 199;  
 Best Local Similarity 97.3%; Pred. No. 1.3e-83;  
 Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 61
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAI 71

QY     62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 131

QY    122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
      ||||||||||||||||||||||||:||||||| |||||||||:|||||||||
Db    132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

QY    182 PGLKRKAD 189
      |||||||:
Db    192 PGLKRKAE 199
  
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RESULT 15

US-10-660-946-1

; Sequence 1, Application US/10660946

; Publication No. US20040063131A1

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; Au-Young, Janice

; Goli, Surya K.

; Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/660,946

; FILING DATE: 12-Sep-2003

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/228,213A

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/700,607

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:



```

;          TELEPHONE: 415-855-0555
;          TELEFAX: 415-845-4166
;  INFORMATION FOR SEQ ID NO: 1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 199 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: peptide
;    IMMEDIATE SOURCE:
;      LIBRARY: <Unknown>
;      CLONE: Consensus
;    SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-660-946-1

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Query Match          97.7%;  Score 904;  DB 12;  Length 199;
Best Local Similarity 97.3%;  Pred. No. 1.3e-83;
Matches 183;  Conservative 3;  Mismatches 2;  Indels 0;  Gaps 0;

```

```

Qy      2  VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12  VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy      62  QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAVL 121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72  QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVL 131

Qy      122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
          ||||||||||||||||||||||||:||||||| |||||||||:||||||||||
Db      132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy      182 PGLKRKAD 189
          |||||||:
Db      192 PGLKRKAE 199

```

```

Search completed: September 29, 2004, 18:48:12
Job time : 21.2878 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:06:43 ; Search time 14.8689 Seconds  
(without alignments)  
4010.587 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWWDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRRKAD 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_cheap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

%  
Result Query  
No. Score Match Length DB ID Description  
-----

1	917	99.1	578	11	Q80W95	Q80w95 mus musculu
2	917	99.1	639	11	Q8K290	Q8k290 mus musculu
3	917	99.1	1046	11	Q8BGK7	Q8bgk7 mus musculu
4	917	99.1	1162	11	Q8BGM9	Q8bgm9 mus musculu
5	914	98.8	375	11	Q8BHF5	Q8bhf5 mus musculu
6	913	98.7	356	11	Q8BH78	Q8bh78 mus musculu
7	908	98.2	986	4	Q8IUA4	Q8iua4 homo sapien
8	906.5	98.0	1163	11	Q8K3G8	Q8k3g8 mus musculu
9	905	97.8	392	4	Q96B16	Q96b16 homo sapien
10	902.5	97.6	357	11	Q8K3G7	Q8k3g7 mus musculu
11	878	94.9	184	6	Q7YRW9	Q7yrw9 bos taurus
12	872	94.3	199	13	Q7T224	Q7t224 gallus gall
13	844	91.2	179	6	Q9GM33	Q9gm33 macaca fasc
14	733	79.2	214	13	Q7T222	Q7t222 carassius a
15	679	73.4	199	4	Q9BQ59	Q9bq59 homo sapien
16	678	73.3	780	11	Q8K4S4	Q8k4s4 mus musculu
17	678	73.3	780	11	Q8K0T0	Q8k0t0 mus musculu
18	669	72.3	760	13	Q90638	Q90638 gallus gall
19	665	71.9	208	13	Q90637	Q90637 gallus gall
20	665	71.9	267	11	Q63765	Q63765 rattus sp.
21	622.5	67.3	236	11	Q8VBU0	Q8vbu0 rattus norv
22	622.5	67.3	237	11	Q8C6D5	Q8c6d5 mus musculu
23	621.5	67.2	643	11	Q8CCU2	Q8ccu2 mus musculu
24	581	62.8	221	13	Q7ZUD6	Q7zud6 brachydanio
25	521	56.3	224	5	Q9VMW1	Q9vmw1 drosophila
26	520	56.2	222	5	Q9VMW4	Q9vmw4 drosophila
27	520	56.2	234	5	Q9VMW3	Q9vmw3 drosophila
28	520	56.2	595	5	Q9VMV9	Q9vmv9 drosophila
29	518	56.0	202	5	Q9VMW2	Q9vmw2 drosophila
30	344	37.2	107	13	Q7T223	Q7t223 carassius a
31	321	34.7	2484	5	Q9U347	Q9u347 caenorhabdi
32	321	34.7	2607	5	Q23187	Q23187 caenorhabdi
33	320	34.6	222	5	Q23188	Q23188 caenorhabdi
34	198.5	21.5	154	5	Q9VIB7	Q9vib7 drosophila
35	198.5	21.5	158	5	Q24199	Q24199 drosophila
36	194	21.0	255	10	O82352	O82352 arabidopsis
37	189	20.4	255	10	Q9SH59	Q9sh59 arabidopsis
38	182	19.7	271	10	Q9SUT9	Q9sut9 arabidopsis
39	170	18.4	257	10	Q9FFS0	Q9ffs0 arabidopsis
40	163	17.6	275	10	Q9SUR3	Q9sur3 arabidopsis
41	160	17.3	200	10	Q9LT71	Q9lt71 arabidopsis
42	158	17.1	200	10	Q8LAT8	Q8lat8 arabidopsis
43	158	17.1	279	10	Q9AWY7	Q9awy7 oryza sativ
44	154.5	16.7	192	10	Q7XR59	Q7xr59 oryza sativ
45	154	16.6	253	10	Q8S2K0	Q8s2k0 oryza sativ

# ALIGNMENTS

## RESULT 1

Q80W95

ID Q80W95 PRELIMINARY; PRT; 578 AA.

AC Q80W95;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Nogo-A (Fragment).  
 GN NOGO-A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tozaki H., Hirata T.;  
 RT "The partial sequence of mouse nogo-A cDNA clone#4109."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB073672; BAC75974.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 99.1%; Score 917; DB 11; Length 578;  
 Best Local Similarity 98.9%; Pred. No. 2.5e-72;  
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 390 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQA 449  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 450 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 509  
 Qy 121 LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 510 LMWVFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 569  
 Qy 181 IPGLKRKAD 189  
 |||||||:  
 Db 570 IPGLKRKAE 578

# RESULT 2

Q8K290

ID Q8K290 PRELIMINARY; PRT; 639 AA.  
 AC Q8K290;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN RTN4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC032192; AAH32192.1; -.  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 99.1%; Score 917; DB 11; Length 639;  
 Best Local Similarity 98.9%; Pred. No. 2.8e-72;  
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 451 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 510  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 511 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDSLKFAV 570  
 Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 571 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 630  
 Qy 181 IPGLKRRKAD 189  
 |||||||:  
 Db 631 IPGLKRRKAE 639

# RESULT 3

## Q8BGK7

ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.  
 AC Q8BGK7;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE RTN4.  
 GN RTN4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RA Oertle T., Schwab M.E.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7;  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SvcJ7;  
 RA Van der Putten H., Mir A.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY102280; AAM73502.1; -.  
 DR EMBL; AY102286; AAM73507.1; -.  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 99.1%; Score 917; DB 11; Length 1046;  
 Best Local Similarity 98.9%; Pred. No. 4.9e-72;  
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 858 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 917  
 QY 61 IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 918 IQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 977  
 QY 121 LMWVFITYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 978 LMWVFITYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1037  
 QY 181 IPGLKRKAD 189  
 |||||||:  
 Db 1038 IPGLKRKAE 1046

#### RESULT 4

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.  
 AC Q8BGM9;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE RTN4.  
 GN RTN4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RA Oertle T., Schwab M.E.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7;  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SvcJ7;  
 RA Van der Putten H., Mir A.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY102284; AAM73506.1; -.  
 DR EMBL; AY102286; AAM73511.1; -.  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 1162 AA; 126613 MW; 855697FBEE11781F CRC64;

Query Match 99.1%; Score 917; DB 11; Length 1162;  
 Best Local Similarity 98.9%; Pred. No. 5.5e-72;  
 Matches 187; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60  
 |||  
 Db 974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 1033  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 |||  
 Db 1034 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1093  
 Qy 121 LMWVFTYVVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 |||  
 Db 1094 LMWVFTYVVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1153  
 Qy 181 IPGLKRKAD 189  
 |||  
 Db 1154 IPGLKRKAE 1162

# RESULT 5

Q8BHF5

ID Q8BHF5 PRELIMINARY; PRT; 375 AA.  
 AC Q8BHF5;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE RTN4.

GN RTN4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7, and 129SvcJ7;  
 RA Oertle T., Schwab M.E.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvcJ7;  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SvcJ7;  
 RA Van der Putten H., Mir A.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY102282; AAM73504.1; -.  
 DR EMBL; AY102286; AAM73509.1; -.  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 98.8%; Score 914; DB 11; Length 375;  
 Best Local Similarity 98.4%; Pred. No. 2.8e-72;  
 Matches 186; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
 :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 187 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 246  
 Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 247 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 306  
 Qy 121 LMWVFTYVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 307 LMWVFTYVGALFENGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 366  
 Qy 181 IPGLKRKAD 189  
 |||||||:  
 Db 367 IPGLKRKAE 375



08BH78

Query Match 98.7%; Score 913; DB 11; Length 356;  
Best Local Similarity 98.9%; Pred. No. 3.3e-72;  
Matches 186; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	2	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI	61
Db	169	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI	228
QY	62	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFVAVL	121
Db	229	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFVAVL	288

Qy 122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181  
 |||  
 Db 289 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 348  
 Qy 182 PGLKRKAD 189  
 |||  
 Db 349 PGLKRKAE 356

RESULT 7

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.  
 AC Q8IUA4;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE RNT4 (RTN4).  
 GN RTN4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., Schwab M.E.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=22376540; PubMed=12488097;  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL J. Mol. Biol. 325:299-323(2003).  
 DR EMBL; AY102285; AAM64244.1; -.  
 DR EMBL; AY123245; AAM64249.1; -.  
 DR EMBL; AY123246; AAM64250.1; -.  
 DR EMBL; AY123247; AAM64251.1; -.  
 DR EMBL; AY123248; AAM64252.1; -.  
 DR EMBL; AY123249; AAM64253.1; -.  
 DR EMBL; AY123250; AAM64254.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 98.2%; Score 908; DB 4; Length 986;  
Best Local Similarity 97.4%; Pred. No. 2.8e-71;  
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY      1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
          |||
Db      798 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 857

QY      61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLVDLKFV 120
          |||
Db      858 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVDLKFV 917

QY      121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
          |||
Db      918 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 977

QY      181 IPGLKRKAD 189
          |||
Db      978 IPGLKRKAE 986
```

RESULT 8

Q8K3G8

ID Q8K3G8 PRELIMINARY; PRT; 1163 AA.  
AC Q8K3G8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Nogo-A.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Jin W., Long M., Li R., Ju G.;  
RT "Cloning and expression of the mouse Nogo-A protein."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY114152; AAM77068.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1163 AA; 126691 MW; 6B5F362799417EA4 CRC64;

Query Match 98.0%; Score 906.5; DB 11; Length 1163;  
Best Local Similarity 98.4%; Pred. No. 4.6e-71;  
Matches 187; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```
QY      1 SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQ 59
          |||
Db      974 SVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQ 1033
```

QY 60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFA 119  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1034 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFA 1093

QY 120 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 179  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1094 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQA 1153

QY 180 KIPGLKRKAD 189  
 ||||||||:  
 Db 1154 KIPGLKRKAE 1163

RESULT 9

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.  
 AC Q96B16;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein (RTN4).  
 GN RTN4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., Schwab M.E.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22376540; PubMed=12488097;  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL J. Mol. Biol. 325:299-323(2003).  
 DR EMBL; BC016165; AAH16165.1; -.  
 DR EMBL; AY102285; AAM64242.1; -.  
 DR EMBL; AY102278; AAM64247.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.

DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 97.8%; Score 905; DB 4; Length 392;  
Best Local Similarity 96.8%; Pred. No. 1.8e-71;  
Matches 183; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60  
:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 204 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 263  
  
Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLVDLKFV 120  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 264 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVDLKFV 323  
  
Qy 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 324 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 383  
  
Qy 181 IPGLKRRKAD 189  
|||||||:  
Db 384 IPGLKRRKAE 392

#### RESULT 10

Q8K3G7

ID Q8K3G7 PRELIMINARY; PRT; 357 AA.  
AC Q8K3G7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Nogo-B.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Jin W., Li R., Long M., Shen J., Ju G.;  
RT "Cloning and expression of the mouse Nogo-B protein."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY114153; AAM77069.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 97.6%; Score 902.5; DB 11; Length 357;  
Best Local Similarity 98.4%; Pred. No. 2.8e-71;

Matches 186; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```
Qy      2 VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 60
      ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
Db     169 VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQA 228

Qy     61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120
      ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
Db    229 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 288

Qy    121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
      ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
Db    289 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 348

Qy    181 IPGLKRKAD 189
      |||||||:
Db    349 IPGLKRKAE 357
```

RESULT 11

Q7YRW9

```
ID   Q7YRW9      PRELIMINARY;      PRT;   184 AA.
AC   Q7YRW9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4w (Fragment).
GN   RTN4.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
DR   EMBL; AY164744; AAP47319.1; -.
FT   NON_TER      1      1
SQ   SEQUENCE    184 AA;  20671 MW;  DE990E03BBAF84A1 CRC64;
```

Query Match 94.9%; Score 878; DB 6; Length 184;  
Best Local Similarity 96.2%; Pred. No. 1.9e-69;  
Matches 177; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy      6 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQAIQKSD 65
      ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
Db      1 LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIIQAIQKSD 60

Qy     66 EGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVF 125
      ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||
Db     61 EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF 120

Qy    126 TYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLK 185
```

```

          |||:|||||:|||||
Db      121 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 180
Qy      186 RKAD 189
          |||:
Db      181 RKA 184

```

RESULT 12

Q7T224

```

ID      Q7T224      PRELIMINARY;      PRT;      199 AA.
AC      Q7T224;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RTN4-C.
GN      RTN4.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22715887; PubMed=12832288;
RA      Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT      "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT      RTN/Nogo gene family.";
RL      FASEB J. 17:1238-1247(2003).
DR      EMBL; AY164737; AAP47312.1; -.
SQ      SEQUENCE      199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

```

```

Query Match      94.3%; Score 872; DB 13; Length 199;
Best Local Similarity 91.5%; Pred. No. 6.9e-69;
Matches 172; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy      2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 71

Qy      62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 121
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      72 QKSDEGHPFRAYLES DVAVSEDLIQKYSSVVLGHINGTVKELRRLFLVDDLVDLSLKFAVL 131

Qy      122 MWVFETYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      132 MWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLVKNVKNVDAMAKIQAKI 191

Qy      182 PGLKRKAD 189
          |||||:
Db      192 PGLKRKTE 199

```

RESULT 13

Q9GM33

```

ID      Q9GM33      PRELIMINARY;      PRT;      179 AA.
AC      Q9GM33;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS *Macaca fascicularis* (Crab eating macaque) (*Cynomolgus* monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; *Macaca*.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 RT libraries.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB049853; BAB16739.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 91.2%; Score 844; DB 6; Length 179;  
 Best Local Similarity 95.5%; Pred. No. 1.8e-66;  
 Matches 171; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 11 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPF 70  
 :|||||||||||||||||||||||||||||||||||||||||:|||||||||||||||  
 Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIAIQKSDEGHPF 60  
 Qy 71 RAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGA 130  
 ||||||||||||||||||||||||| |||||||||||||:|||||||||||||||  
 Db 61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLRFVLMWVFTYVGA 120  
 Qy 131 LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 189  
 |||||||||||||||||:||||||| |||||||||:|||||||||||||||:|||||||  
 Db 121 LFNGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

# RESULT 14

Q7T222

ID Q7T222 PRELIMINARY; PRT; 214 AA.  
 AC Q7T222;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE RTN4-M.  
 GN RTN4.  
 OS *Carassius auratus* (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; *Carassius*.  
 OX NCBI\_TaxID=7957;  
 RN [1]





DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS00047; HISTONE\_H4; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

Query Match 73.4%; Score 679; DB 4; Length 199;  
 Best Local Similarity 67.9%; Pred. No. 6.6e-52;  
 Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

```

Qy      3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
          :|||||||:|:|:|:| | | | | | | | | | | | | | | | | | | | | | |
Db      13 IDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy      63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLM 122
          |:|||||:|||| |: |:| :|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|
Db      73 KTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLM 132

Qy     123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
          |: |||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     133 WLLTYVGALFNGLTLLLMVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 192

Qy     183 GLKRRKAD 189
          | | | |:
Db     193 GAKRHAE 199
  
```

Search completed: September 29, 2004, 18:19:40  
 Job time : 15.8689 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:04:48 ; Search time 2.70944 Seconds  
(without alignments)  
3632.211 Million cell updates/sec

Title: US-09-830-972-2\_COPY\_975\_1163  
Perfect score: 925  
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRRKAD 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	925	100.0	1163	1	RTN4_RAT	Q9jkl1 rattus norv
2	913	98.7	199	1	RTN4_MOUSE	Q99p72 mus musculu
3	908	98.2	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
4	679	73.4	776	1	RTN1_HUMAN	Q16799 homo sapien
5	678	73.3	777	1	RTN1_RAT	Q64548 rattus norv
6	622.5	67.3	236	1	RTN3_HUMAN	O95197 homo sapien
7	622.5	67.3	237	1	RTN3_MOUSE	Q9es97 mus musculu
8	475	51.4	545	1	RTN2_HUMAN	O75298 homo sapien
9	472	51.0	471	1	RTN2_MOUSE	O70622 mus musculu
10	94	10.2	468	1	ACH5_HUMAN	P30532 homo sapien
11	92.5	10.0	197	1	AR61_DROME	Q9ves1 drosophila
12	88.5	9.6	1278	1	NPC1_HUMAN	O15118 homo sapien
13	86.5	9.4	578	1	MDLB_BUCBP	Q89a96 buchnera ap
14	86	9.3	589	1	Y015_MYCGE	P47261 mycoplasma
15	85.5	9.2	296	1	YBZ7_YEAST	P38279 saccharomyc
16	85	9.2	299	1	Y779_METJA	Q58189 methanococc
17	83.5	9.0	570	1	SECD_STRCO	Q53955 streptomyce

18	83	9.0	388	1	YUBA_BACSU	032086	bacillus su
19	82.5	8.9	502	1	OXAA_AQUAE	066561	aquifex aeo
20	82	8.9	744	1	PRES_RAT	Q9eph0	rattus norv
21	81.5	8.8	499	1	UBPG_YEAST	Q02863	saccharomyc
22	81.5	8.8	580	1	MDLB_BUCAI	P57552	buchnera ap
23	81.5	8.8	839	1	TLR4_PANPA	Q9ttn0	pan paniscu
24	81	8.8	607	1	GLMS_AGRT5	Q8ueh1	a glucosami
25	81	8.8	744	1	PRES_MERUN	Q9jkq2	meriones un
26	81	8.8	744	1	PRES_MOUSE	Q99nh7	mus musculu
27	79.5	8.6	324	1	MRAY_LISIN	Q929y0	listeria in
28	79.5	8.6	470	1	YMP8_CAEEL	P53993	caenorhabdi
29	79.5	8.6	592	1	Y036_HAEIN	Q57335	haemophilus
30	79	8.5	556	1	NU2M_PODAN	P15578	podospora a
31	78.5	8.5	748	1	TAP1_HUMAN	Q03518	homo sapien
32	78	8.4	284	1	HTPX_METJA	Q59076	methanococc
33	78	8.4	660	1	SGAT_MYCPN	P75291	mycoplasma
34	78	8.4	744	1	PRES_HUMAN	P58743	homo sapien
35	78	8.4	993	1	NISB_LACLA	P20103	lactococcus
36	77.5	8.4	503	1	C72R_ARATH	Q9sae1	arabidopsis
37	77.5	8.4	780	1	FTSK_SPOUR	Q9rnv1	sporosarcin
38	77.5	8.4	1277	1	NPC1_PIG	P56941	sus scrofa
39	77	8.3	329	1	O5T2_HUMAN	Q8ngg2	homo sapien
40	77	8.3	839	1	TLR4_HUMAN	O00206	homo sapien
41	76.5	8.3	526	1	ERGL_HUMAN	Q9hat1	homo sapien
42	76	8.2	312	1	OLF2_CHICK	P37068	gallus gall
43	76	8.2	666	1	NU5M_CHOCR	P48920	chondrus cr
44	75.5	8.2	221	1	YA78_AQUAE	O67171	aquifex aeo
45	75.5	8.2	554	1	PIGS_HUMAN	Q96s52	homo sapien

#### ALIGNMENTS

##### RESULT 1

##### RTN4\_RAT

ID RTN4\_RAT STANDARD; PRT; 1163 AA.  
 AC Q9JK11; Q9JK10; Q9ROD9; Q9WUE9; Q9WUF0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)  
 DE (Glut4 vesicle 20 kDa protein).  
 GN RTN4 OR NOGO.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
 RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
 RX MEDLINE=99249816; PubMed=10231557;  
 RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;  
 RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:  
 RT a new member of the reticulon family."  
 RL Biochim. Biophys. Acta 1450:68-76(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=20129258; PubMed=10667796;  
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
 RA Spillmann A.A., Christ F., Schwab M.E.;  
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
 RT antigen for monoclonal antibody IN-1.";  
 RL Nature 403:434-439(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
 RA Ito T., Schwartz S.M.;  
 RT "Cloning of a member of the reticulon gene family in rat: one of two  
 RT minor splice variants.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=22033691; PubMed=12037567;  
 RA GrandPre T., Li S., Strittmatter S.M.;  
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
 RL Nature 417:547-551(2002).  
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
 CC membrane of the endoplasmic reticulum through 2 putative  
 CC transmembrane domains (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=Nogo-A, NI-220-250;  
 CC IsoId=Q9JK11-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;  
 CC IsoId=Q9JK11-2; Sequence=VSP\_005658;  
 CC Name=3; Synonyms=Nogo-C, VP20;  
 CC IsoId=Q9JK11-3; Sequence=VSP\_005656, VSP\_005657;  
 CC Name=4; Synonyms=Foocen-M2;  
 CC IsoId=Q9JK11-4; Sequence=VSP\_005659;  
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic  
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are  
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells  
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,  
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high  
 CC level in skeletal muscle. In adult animals isoform 1 is expressed  
 CC mainly in the nervous system.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF051335; AAF01564.1; -.  
 DR EMBL; AJ242961; CAB71027.1; -.  
 DR EMBL; AJ242962; CAB71028.1; -.

DR EMBL; AJ242963; CAB71029.1; -.  
 DR EMBL; AF132045; AAD31019.1; -.  
 DR EMBL; AF132046; AAD31020.1; -.  
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.  
 DR GO; GO:0005635; C:nuclear membrane; ISS.  
 DR GO; GO:0005515; F:protein binding; ISS.  
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.  
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).  
 FT TRANSMEM 990 1010 POTENTIAL.  
 FT DOMAIN 1011 1104 LUMENAL (Potential).  
 FT TRANSMEM 1105 1125 POTENTIAL.  
 FT DOMAIN 1126 1163 CYTOPLASMIC (Potential).  
 FT DOMAIN 976 1163 RETICULON.  
 FT DOMAIN 33 46 POLY-GLU.  
 FT DOMAIN 73 76 POLY-ALA.  
 FT DOMAIN 140 145 POLY-PRO.  
 FT VARSPLIC 1 964 Missing (in isoform 3).  
 FT /FTId=VSP\_005656.  
 FT VARSPLIC 965 975 AVLSAELSKTS -> MDGQKKHWKDK (in isoform 3).  
 FT /FTId=VSP\_005657.  
 FT VARSPLIC 173 975 Missing (in isoform 2).  
 FT /FTId=VSP\_005658.  
 FT VARSPLIC 192 975 Missing (in isoform 4).  
 FT /FTId=VSP\_005659.  
 FT CONFLICT 1130 1131 MISSING (IN REF. 3; AAD31020).  
 SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

Query Match 100.0%; Score 925; DB 1; Length 1163;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-68;  
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 975 SVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 1034  
 QY 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 1094  
 QY 121 LMWVFITYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1095 LMWVFITYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154  
 QY 181 IPGLKRKAD 189  
 ||||||||  
 Db 1155 IPGLKRKAD 1163

# RESULT 2

RTN4\_MOUSE

ID RTN4\_MOUSE STANDARD; PRT; 199 AA.

AC Q99P72; Q9CTE3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).  
 GN RTN4 OR NOGO.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=3T3-L1; TISSUE=Adipocyte;  
 RA Coulson A.C., Craggs P.D., Morris N.J.;  
 RT "Mouse vp20/RTN4C cDNA."  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE OF 170-199 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
 CC membrane of the endoplasmic reticulum through 2 putative  
 CC transmembrane domains (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=1;  
 CC Comment=A number of isoforms may be produced;  
 CC Name=1;  
 CC IsoId=Q99P72-1; Sequence=Displayed;  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)  
 DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
 DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).  
 GN RTN4 OR NOGO OR ASY OR KIAA0886.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=20129242; PubMed=10667780;  
 RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
 RA Michalovich D., Simmons D.L., Walsh F.S.;  
 RT "Inhibitor of neurite outgrowth in humans.";  
 RL Nature 403:383-384(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=21010696; PubMed=11126360;  
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";  
 RL Oncogene 19:5736-5746(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=20237542; PubMed=10773680;  
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
 RT 2p14-->2p13 by radiation hybrid mapping.";  
 RL Cytogenet. Cell Genet. 88:101-102(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RA Jin W.-L., Ju G.;  
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
 RC TISSUE=Placenta, and Skeletal muscle;  
 RA Ito T., Schwartz S.M.;  
 RT "Cloning of a member of the reticulon gene family in human.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Fibroblast;  
 RA Yutsudo M.;  
 RT "Isolation of a cell death-inducing gene.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Pituitary;  
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
 RA Luo B., Hu R., Chen J.;  
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,

RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
 RA Yu J., Han L.H.;  
 RT "Novel human cDNA clone with function of inhibiting cancer cell  
 RT growth.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=99156230; PubMed=10048485;  
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 5:355-364(1998).  
 RN [10]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RX MEDLINE=20499367; PubMed=11042152;  
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 RN [12]  
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
 RC TISSUE=Brain;  
 RA Mao Y.M., Xie Y., Zheng Z.H.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [13]  
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).  
 RC TISSUE=Testis;

RA Sha J.H., Zhou Z.M., Li J.M.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [14]  
 RP TOPOLOGY.  
 RC TISSUE=Brain;  
 RX MEDLINE=20129259; PubMed=10667797;  
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
 RT "Identification of the Nogo inhibitor of axon regeneration as a  
 RT Reticulon protein.";  
 RL Nature 403:439-444(2000).  
 RN [15]  
 RP FUNCTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=21069055; PubMed=11201742;  
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;  
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal  
 RT regeneration.";  
 RL Nature 409:341-346(2001).  
 RN [16]  
 RP REVIEW.  
 RX MEDLINE=21888956; PubMed=11891768;  
 RA Ng C.E.L., Tang B.L.;  
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron  
 RT regeneration.";  
 RL J. Neurosci. Res. 67:559-565(2002).  
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults.  
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.  
 CC This is likely consecutive to their change in subcellular  
 CC location, from the mitochondria to the endoplasmic reticulum,  
 CC after binding and sequestration.  
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
 CC through 2 putative transmembrane domains.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;  
 CC IsoId=Q9NQC3-1; Sequence=Displayed;  
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;  
 CC IsoId=Q9NQC3-2; Sequence=VSP\_005655;  
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;  
 CC IsoId=Q9NQC3-3; Sequence=VSP\_005652, VSP\_005653;  
 CC Name=4;  
 CC IsoId=Q9NQC3-4; Sequence=VSP\_005654;  
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
 CC widely expressed excepted for the liver. Isoform 3 is expressed in  
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
 CC specific.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to  
 CC frameshifts in positions 1149 and 1156.  
 CC -----  
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OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).  
 RC TISSUE=Lung carcinoma;  
 RX MEDLINE=93293865; PubMed=7685762;  
 RA Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,  
 RA Ramaekers F.C.S., Van de Ven W.J.M.;  
 RT "Cloning and expression of alternative transcripts of a novel  
 RT neuroendocrine-specific gene and identification of its 135-kDa  
 RT translational product.";  
 RL J. Biol. Chem. 268:13439-13447(1993).  
 RN [2]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=96429995; PubMed=8833145;  
 RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,  
 RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;  
 RT "Genomic organization of the human NSP gene, prototype of a novel gene  
 RT family encoding reticulons.";  
 RL Genomics 32:191-199(1996).  
 RN [3]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=98228245; PubMed=9560466;  
 RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,  
 RA Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;  
 RT "Neuronal differentiation is accompanied by NSP-C expression.";  
 RL Cell Tissue Res. 292:229-237(1998).  
 CC -!- FUNCTION: May be involved in neuroendocrine secretion or in  
 CC membrane trafficking in neuroendocrine cells.  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=RTN1-A; Synonyms=NSP-A;  
 CC IsoId=Q16799-1; Sequence=Displayed;  
 CC Name=RTN1-B; Synonyms=NSP-B;  
 CC IsoId=Q16799-2; Sequence=VSP\_005644;  
 CC Name=RTN1-C; Synonyms=NSP-C;  
 CC IsoId=Q16799-3; Sequence=VSP\_005645, VSP\_005646;  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES  
 CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C  
 CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.  
 CC -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L10333; AAA59950.1; -.  
 DR EMBL; L10334; AAA59951.1; -.  
 DR EMBL; L10335; AAA59952.1; -.  
 DR PIR; A46583; A46583.  
 DR PIR; I60904; I60904.  
 DR Genew; HGNC:10467; RTN1.

```

DR      MIM; 600865; -.
DR      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
DR      GO; GO:0004871; F:signal transducer activity; NAS.
DR      GO; GO:0030182; P:neuron differentiation; TAS.
DR      GO; GO:0007165; P:signal transduction; NAS.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW      Phosphorylation.
FT      TRANSMEM      603      623      POTENTIAL.
FT      TRANSMEM      726      746      POTENTIAL.
FT      DOMAIN        589      776      RETICULON.
FT      DOMAIN        609      612      POLY-LEU.
FT      VARSPLIC      1      420      Missing (in isoform RTN1-B).
FT                                          /FTId=VSP_005644.
FT      VARSPLIC      1      568      Missing (in isoform RTN1-C).
FT                                          /FTId=VSP_005645.
FT      VARSPLIC      569      588      GPGPLGPGAPPLLFLNKQK -> MQATADSTKMDCVWSNW
FT                                          KSQ (in isoform RTN1-C).
FT                                          /FTId=VSP_005646.
SQ      SEQUENCE      776 AA; 83617 MW; CA5B6232353096FE CRC64;

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Qy	3	VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ	62
		: :       : : : :            : :     : :                : : :	
Db	590	IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAAALSATISFRIYKSVLQAVQ	649
Qy	63	KSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDLDVDSLKFVLM	122
		: :     : :     :  : :   : : :   : : :	
Db	650	KTDEGHPPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLDSLKFVLM	709
Qy	123	WVFYYVGALFNGLTLILLALISLESIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP	182
		:	
Db	710	WLLTYVGALFNGLTLILLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP	769
Qy	183	GLKRKAD	189
		:	
Db	770	GAKRHAE	776

## RESULT 5

```

RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC      STRAIN=Wistar; TISSUE=Brain cortex;
RX      MEDLINE=96386034; PubMed=8793864;
RA      Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA      Georgiev G.P., Buchman V.L.;
RT      "Intracellular compartmentalization of two differentially spliced s-
RT      rex/NSP mRNAs in neurons.";
RL      Mol. Cell. Neurosci. 7:289-303(1996).
CC      -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC      membrane trafficking in neuroendocrine cells.
CC      -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
CC      similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=RTN1-B; Synonyms=S-RexB;
CC      IsoId=Q64548-1; Sequence=Displayed;
CC      Name=RTN1-S; Synonyms=S-RexS;
CC      IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC      -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC      PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC      HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC      EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC      TYPES.
CC      -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC      HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC      DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC      THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC      DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC      HINDBRAIN.
CC      -!- SIMILARITY: Contains 1 reticulon domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U17604; AAC53046.1; -.
DR      EMBL; U17603; AAC53045.1; -.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      TRANSMEM      604      624      POTENTIAL.
FT      TRANSMEM      727      747      POTENTIAL.
FT      DOMAIN        590      777      RETICULON.
FT      DOMAIN        610      613      POLY-LEU.
FT      VARSPLIC       1      569      Missing (in isoform RTN1-S).
FT                                     /FTId=VSP_005647.
FT      VARSPLIC      570      589      IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
FT      KSQ (in isoform RTN1-S).
FT      /FTId=VSP_005648.
SQ      SEQUENCE      777 AA;  83001 MW;  AF7479C50F28D0AC CRC64;

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Query Match 73.3%; Score 678; DB 1; Length 777;  
Best Local Similarity 67.4%; Pred. No. 1.9e-48;  
Matches 126; Conservative 32; Mismatches 29; Indels 0; Gaps 0;

Qy	3	VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVITQAIQ	62
Db	591	IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAAALSATISFRIYKSVLQAVQ	650
Qy	63	KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLM	122
Db	651	KTDEGHPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKELRRLFLVQDLVDLSLKFAVLM	710
Qy	123	WVFTYVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP	182
Db	711	WLLTYVGALFENGLTLLLMAVVSMFTLPVVYVKHQAVDQYLGIVRTHINTVVAKIQAKIP	770
Qy	183	GLKRKAD	189
Db	771	GAKRHAE	777

RESULT 6

RTN3 HUMAN

ID RTN3 HUMAN STANDARD; PRT; 236 AA.

AC 095197;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like

DE protein II) (NSPLII).

GN RTN3 OR NSPL2.

OS Homo sapiens (Human) .

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC TISSUE=Retina;

RX MEDLINE=99265974; PubMed=10331947;

RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;

BT "Cloning of a novel member of the reticulon gene family (RTN3): gene

RT structure and chromosomal localization to 11q13.";

RL Genomics 58:73-81(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;

RT "Cloning and expression analysis of a cDNA encoding a novel

RT neuroendocrine-specific protein-like protein 1: NSPL1.";

RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain, Eye, and Lymph;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,



RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum (Potential).  
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN  
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL  
 CC RETINA.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF059524; AAC99319.1; -.  
 DR EMBL; AF059529; AAD20951.1; -.  
 DR EMBL; AF059525; AAD20951.1; JOINED.  
 DR EMBL; AF059526; AAD20951.1; JOINED.  
 DR EMBL; AF059527; AAD20951.1; JOINED.  
 DR EMBL; AF059528; AAD20951.1; JOINED.  
 DR EMBL; AF119297; AAD26810.1; -.  
 DR EMBL; BC000634; AAH00634.1; -.  
 DR EMBL; BC010556; AAH10556.1; -.  
 DR EMBL; BC011394; AAH11394.1; -.  
 DR EMBL; BC022993; AAH22993.1; -.  
 DR Genew; HGNC:10469; RTN3.  
 DR MIM; 604249; -.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Transmembrane; Endoplasmic reticulum.  
 FT TRANSMEM 68 88 POTENTIAL.  
 FT TRANSMEM 177 197 POTENTIAL.  
 FT DOMAIN 48 236 RETICULON.  
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCD7B7 CRC64;

Query Match 67.3%; Score 622.5; DB 1; Length 236;  
 Best Local Similarity 59.5%; Pred. No. 2.1e-44;  
 Matches 113; Conservative 41; Mismatches 35; Indels 1; Gaps 1;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
 :| ||:||||:|||| ||| :| :||| ||:|| :| : ||||| ||||| ||||  
 Db 47 AVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVSVSYLILALLSVTISFRIYKSVQA 106

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAV 120  
 :|||:||||:|||| : :| | | :| :| :| : ||||:||||| ||  
 Db 107 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 166

Qy 121 LMWVFTYVVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||: ||||:||||:|||| : :||:|:|:|:| : ||||:|:| | : |||||  
 Db 167 FMWLMTYVGA VENGITLLILAELLIFSVPVYKYEKYKTQIDHYVGIARDQTKSIVEKIQAK 226

Qy 181 IPGL-KRKAD 189  
 :||: |:||:  
 Db 227 LPGIAKKKAE 236

# RESULT 7

## RTN3\_MOUSE

ID RTN3\_MOUSE STANDARD; PRT; 237 AA.  
 AC Q9ES97;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Reticulon protein 3.  
 GN RTN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;  
 RT "Cloning and expression profile of a novel mouse cDNA encoding a human  
 RT RTN3 homolog.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum (Potential).  
 CC -!- SIMILARITY: Contains 1 reticulon domain.

CC -----  
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 CC -----

DR EMBL; AF195940; AAG31360.1; -.  
 DR EMBL; BC014697; AAH14697.1; -.  
 DR MGD; MGI:1339970; Rtn3.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Transmembrane; Endoplasmic reticulum.  
 FT TRANSMEM 69 89 POTENTIAL.  
 FT TRANSMEM 167 187 POTENTIAL.  
 FT DOMAIN 49 237 RETICULON.  
 SQ SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;

Query Match 67.3%; Score 622.5; DB 1; Length 237;  
 Best Local Similarity 59.5%; Pred. No. 2.1e-44;  
 Matches 113; Conservative 41; Mismatches 35; Indels 1; Gaps 1;

QY 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQA 60  
 :| ||::|||:|||| ||| :| :|||| ||::|| :| : |||||:|||||:| ||||  
 Db 48 AVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVSYLILALLSVTISFRVYKSVQA 107  
 QY 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLEFLVDDLVDLSLKFAV 120  
 :|||:||||:||||: :: :| | | :| : ||| :| : ||||:||||| ||  
 Db 108 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHVNKALKLIIRLFLVEDLVDSLKLAV 167  
 QY 121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180  
 ||: ||||:||||:||||| : :||:|::|||: ||||:|:| | : |||||  
 Db 168 FMWLMTYVGAVFNGITLLILAELLVFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 227  
 QY 181 IPGL-KRKAD 189  
 :||: |::|:  
 Db 228 LPGIAKKKAE 237

# RESULT 8

RTN2\_HUMAN

ID RTN2\_HUMAN STANDARD; PRT; 545 AA.

AC O75298; O60509;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like

DE protein 1) (NSPLI).  
 GN RTN2 OR NSPL1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
 RC TISSUE=Lung carcinoma;  
 RX MEDLINE=98360096; PubMed=9693037;  
 RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;  
 RT "cDNA cloning, genomic organization, and expression of the human RTN2  
 RT gene, a member of a gene family encoding reticulons.";  
 RL Genomics 51:98-106(1998).  
 RN [2]  
 RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).  
 RC TISSUE=Brain;  
 RX MEDLINE=98191726; PubMed=9530622;  
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;  
 RT "Molecular cloning of a novel mouse gene with predominant muscle and  
 RT neural expression.";  
 RL Mamm. Genome 9:274-282(1998).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=RTN2-A;  
 CC IsoId=O75298-1; Sequence=Displayed;  
 CC Note=Isoform RTN2-C is produced by alternative initiation at  
 CC Met-341 of isoform RTN2-A;  
 CC Name=RTN2-B;  
 CC IsoId=O75298-2; Sequence=VSP\_005649;  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced  
 CC by alternative initiation at Met-1 and Met-341;  
 CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL  
 CC MUSCLE.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF004222; AAC32542.1; -.  
 DR EMBL; AF004223; AAC32543.1; -.  
 DR EMBL; AF004224; AAC32544.1; -.  
 DR EMBL; AF038540; AAC14910.1; -.  
 DR Genew; HGNC:10468; RTN2.  
 DR MIM; 603183; -.  
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.  
 DR GO; GO:0004871; F:signal transducer activity; NAS.  
 DR GO; GO:0007165; P:signal transduction; NAS.  
 DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;  
 KW Alternative initiation.  
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.  
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.  
 FT INIT\_MET 341 341 FOR ISOFORM RTN2-C.  
 FT TRANSMEM 368 388 POTENTIAL.  
 FT TRANSMEM 463 483 POTENTIAL.  
 FT DOMAIN 345 545 RETICULON.  
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).  
 FT /FTId=VSP\_005649.  
 SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;

Query Match 51.4%; Score 475; DB 1; Length 545;  
 Best Local Similarity 50.5%; Pred. No. 7e-32;  
 Matches 92; Conservative 36; Mismatches 54; Indels 0; Gaps 0;

QY 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 61  
 | | | | | : | : : | | | : | | | | | | : : | | | | | : : | : | :  
 Db 345 VADLLYWKDTRTSGVVFTGLMVSLCLLHFSIVSVAHLALLLLCGTISLRVYRKVLQAV 404  
 QY 62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121  
 : | : | : | : | : : : | : : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 405 HRGDGANPFQAYLDVDLTLTREQTERLSHQITSRVVSAATQLRHFFLVEDLVDSLKLALL 464  
 QY 122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181  
 : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Db 465 FYILTFVGAIFNGLTLLILGVIGLFTIPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKI 524  
 QY 182 PG 183  
 | |  
 Db 525 PG 526

# RESULT 9

## RTN2\_MOUSE

ID RTN2\_MOUSE STANDARD; PRT; 471 AA.  
 AC O70622; O70620;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like  
 DE protein 1) (NSPLI).  
 GN RTN2 OR NSPL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.  
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;  
 RX MEDLINE=98191726; PubMed=9530622;  
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;  
 RT "Molecular cloning of a novel mouse gene with predominant muscle and  
 RT neural expression."  
 RL Mamm. Genome 9:274-282(1998).

RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Retina;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum  
 CC (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Brain;  
 CC IsoId=O70622-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Muscle;  
 CC IsoId=O70622-2; Sequence=VSP\_005650, VSP\_005651;  
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular  
 CC tissues.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF038537; AAC14906.1; -.  
 DR EMBL; AF038537; AAC14907.1; -.  
 DR EMBL; AF038538; AAC14908.1; -.  
 DR EMBL; AF038539; AAC14909.1; -.  
 DR EMBL; AF093624; AAD13195.1; -.  
 DR EMBL; BC031370; AAH31370.1; -.  
 DR MGD; MGI:107612; Rtn2.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
 FT TRANSMEM 295 315 POTENTIAL.  
 FT DOMAIN 272 471 RETICULON.

FT	VARSPLIC	1	267	Missing (in isoform 2).
FT				/FTId=VSP_005650.
FT	VARSPLIC	268	271	PLLL -> MGSK (in isoform 2).
FT				/FTId=VSP_005651.
SO	SEQUENCE	471 AA;	51346 MW;	9BBD8F372CF63AD3 CRC64;

Qy	2	VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI	61
		:   : :     :     :           : :           : :	
Db	272	VADLLYWKDTRTSGAVFTGLMASLLCLLHFSIVSVAHLALLGLCATISLRVYRKVLQAV	331
Qy	62	QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLDVDSLKFAVL	121
		:   :   :   :   : : :   : :       :       :               :	
Db	332	HRGDGTNPFQAYLDMDLTLTREQTERLSQQIASHVNSTATQLRHFFLVEDLDVSLKLALL	391
Qy	122	MWVFETYVGALFENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI	181
		: :   :   :         :   : :   : : : :   :       :   : :       :	
Db	392	FYILTFVGAIFENGLTLVILGVVALFTVPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKI	451
Qy	182	PG 183	
Db	452	PG 453	

RL J. Mol. Neurosci. 7:217-228(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97162233; PubMed=9009220;  
RA Groot Kormelink P.J., Luyten W.H.M.L.;  
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal  
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and  
RT expression of seven nAChR subunits in the human neuroblastoma cell  
RT line SH-SY5Y and/or IMR-32.";  
RL FEBS Lett. 400:309-314(1997).

RN [4]  
RP SEQUENCE FROM N.A.  
RA Duga S., Solda G., Asselta R., Bonati M.T., Dalpra L., Malcovati M.,  
RA Tenchini M.L.;  
RT "Characterization of the genomic structure of human nicotinic  
RT acetylcholine receptor CHRNA5/A3/B4 gene cluster: identification of  
RT two novel introns in the 3' untranslated region of CHRNA3 and of a  
RT tail-to-tail overlap between CHRNA3 and CHRNA5.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an  
CC extensive change in conformation that affects all subunits and  
CC leads to opening of an ion-conducting channel across the plasma  
CC membrane.

CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different type  
CC of subunits: alpha and non-alpha (betaA).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.

CC -----  
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CC -----

DR EMBL; M83712; AAA58357.1; -.  
DR EMBL; U62434; AAB40112.1; -.  
DR EMBL; Y08419; CAA69696.1; -.  
DR EMBL; AJ306481; CAC34820.1; -.  
DR EMBL; AJ306482; CAC34820.1; JOINED.  
DR EMBL; AJ306483; CAC34820.1; JOINED.  
DR EMBL; AJ306484; CAC34820.1; JOINED.  
DR EMBL; AJ306485; CAC34820.1; JOINED.  
DR EMBL; AJ306486; CAC34820.1; JOINED.  
DR EMBL; BC033639; AAH33639.1; -.  
DR PIR; A38223; A38223.  
DR Genew; HGNC:1959; CHRNA5.  
DR MIM; 118505; -.  
DR InterPro; IPR006029; Neu\_channel\_memb.  
DR InterPro; IPR006202; Neur\_chan\_LBD.  
DR InterPro; IPR006201; Neur\_channel.  
DR Pfam; PF02931; Neur\_chan\_LBD; 1.  
DR Pfam; PF02932; Neur\_chan\_memb; 1.  
DR PRINTS; PR00252; NRIONCHANNEL.  
DR TIGRFAMs; TIGR00860; LIC; 1.  
DR PROSITE; PS00236; NEUROTR\_ION\_CHANNEL; 1.  
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;  
KW Transmembrane; Multigene family.

FT	SIGNAL	1	22	POTENTIAL.
FT	CHAIN	23	468	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-5 CHAIN.
FT				EXTRACELLULAR.
FT	DOMAIN	23	249	POTENTIAL.
FT	TRANSMEM	250	274	POTENTIAL.
FT	TRANSMEM	282	299	POTENTIAL.
FT	TRANSMEM	316	337	POTENTIAL.
FT	DOMAIN	338	429	CYTOPLASMIC.
FT	TRANSMEM	430	448	POTENTIAL.
FT	DISULFID	170	184	BY SIMILARITY.
FT	DISULFID	234	235	ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
FT				
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	229	229	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	23	34	RCGLAGAAGGAQ -> ALRSSRARRAAR (IN REF. 1).
FT	CONFLICT	128	128	V -> S (IN REF. 1).
FT	CONFLICT	365	365	C -> S (IN REF. 1).
FT	CONFLICT	398	398	D -> N (IN REF. 2 AND 4).
FT	CONFLICT	405	405	R -> T (IN REF. 1).
SQ	SEQUENCE	468 AA;	53054 MW;	7FE91A2E362289C0 CRC64;

Query Match 10.2%; Score 94; DB 1; Length 468;  
Best Local Similarity 21.5%; Pred. No. 1.5;  
Matches 41; Conservative 32; Mismatches 62; Indels 56; Gaps 7;

Qy 24 LLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVQAIQKSDEGHP- 69  
:|:|||||:| :|: :|:|:| :| :| :|  
Db 288 VLVSLTVFLLVIEEIIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRSSSTHNA 347  
Qy 70 -----FRAYLESEVAISEELVQ----KYSNSALGHVNSTIKELRRLF 107

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|::: | | | : | : : |
Db      348 MAPLVRKIFLHTLPKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALDSIRYITRHI 407
Qy      108 L----VDDLVDLKF-----AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 157
      : |::: | | : : | | : | : | : | :
Db      408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS-----IVGSLGLF-VPVIYKWANI 457
Qy      158 QIDHYLGLANK 168
      | : : | | |
Db      458 LIPVHIGNANK 468

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RESULT 11

AR61\_DROME

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ID  AR61_DROME      STANDARD;      PRT;      197 AA.
AC  Q9VES1;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  ARL-6 interacting protein-1 homolog.
GN  CG10326.
OS  Drosophila melanogaster (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7227;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Berkeley;
RX  MEDLINE=20196006; PubMed=10731132;
RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA  Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA  Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA  Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

```



DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Niemann-Pick C1 protein precursor.  
 GN NPC1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND VARIANTS NPC1.  
 RX MEDLINE=97362323; PubMed=9211849;  
 RA Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D.,  
 RA Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B.,  
 RA Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A.,  
 RA Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R.,  
 RA Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y.,  
 RA Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J.,  
 RA Markie D., O'Neill R.R., van Diggelen O.P., Elleder M.,  
 RA Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.;  
 RT "Niemann-Pick C1 disease gene: homology to mediators of cholesterol  
 RT homeostasis.";  
 RL Science 277:228-231(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANTS.  
 RX MEDLINE=99355599; PubMed=10425213;  
 RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,  
 RA Carstea E.D.;  
 RT "The genomic organization and polymorphism analysis of the human  
 RT Niemann-Pick C1 gene.";  
 RL Biochem. Biophys. Res. Commun. 261:493-498(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21623216; PubMed=11754101;  
 RA Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J.,  
 RA Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.;  
 RT "NPC1: Complete genomic sequence, mutation analysis, and  
 RT characterization of haplotypes.";  
 RL Hum. Mutat. 19:30-38(2002).  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=99128318; PubMed=9927649;  
 RA Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S.,  
 RA Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III;  
 RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and  
 RT lysosomal targeting in cholesterol mobilization.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).  
 RN [5]  
 RP VARIANT NPD TRP-992.  
 RX MEDLINE=98299797; PubMed=9634529;  
 RA Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M.,  
 RA Byers D.M., Dobson M.J., Neumann P.E.;  
 RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a  
 RT G3097-->T transversion in NPC1.";  
 RL Am. J. Hum. Genet. 63:52-54(1998).  
 RN [6]  
 RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; LEU-954; TRP-992; ALA-1007;  
 RP THR-1061 AND VAL-1213.

RX MEDLINE=99452586; PubMed=10521290;  
 RA Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C.,  
 RA Neumann P.E.;  
 RT "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich  
 RT domain.";  
 RL Am. J. Hum. Genet. 65:1252-1260(1999).  
 RN [7]  
 RP VARIANT NPC1 THR-1061.  
 RX MEDLINE=99452593; PubMed=10521297;  
 RA Millat G., Marçais C., Rafi M.A., Yamamoto T., Morris J.A.,  
 RA Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.;  
 RT "Niemann-Pick C1 disease: the I1061T substitution is a frequent mutant  
 RT allele in patients of Western European descent and correlates with a  
 RT classic juvenile phenotype.";  
 RL Am. J. Hum. Genet. 65:1321-1329(1999).  
 RN [8]  
 RP VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.  
 RX MEDLINE=99408226; PubMed=10480349;  
 RA Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,  
 RA Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A.,  
 RA Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,  
 RA Ohno K.;  
 RT "NPC1 gene mutations in Japanese patients with Niemann-Pick disease  
 RT type C.";  
 RL Hum. Genet. 105:10-16(1999).  
 RN [9]  
 RP VARIANTS NPC1 GLN-958 AND ALA-1007.  
 RX MEDLINE=21313111; PubMed=11349231;  
 RA Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F.,  
 RA Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.;  
 RT "Niemann-Pick C variant detection by altered sphingolipid trafficking  
 RT and correlation with mutations within a specific domain of NPC1.";  
 RL Am. J. Hum. Genet. 68:1361-1372(2001).  
 RN [10]  
 RP VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.  
 RX MEDLINE=21313105; PubMed=11333381;  
 RA Millat G., Marçais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K.,  
 RA Wenger D.A., Ohno K., Vanier M.T.;  
 RT "Niemann-Pick C1 disease: correlations between NPC1 mutations, levels  
 RT of NPC1 protein, and phenotypes emphasize the functional significance  
 RT of the putative sterol-sensing domain and of the cysteine-rich  
 RT luminal loop.";  
 RL Am. J. Hum. Genet. 68:1373-1385(2001).  
 RN [11]  
 RP VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.  
 RX MEDLINE=21372069; PubMed=11479732;  
 RA Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T.,  
 RA Millat G.;  
 RT "Niemann-Pick type C disease: NPC1 mutations associated with severe  
 RT and mild cellular cholesterol trafficking alterations.";  
 RL Hum. Genet. 109:24-32(2001).  
 CC -!- FUNCTION: Involved in the intracellular trafficking of  
 CC cholesterol. May play a role in vesicular trafficking in glia, a  
 CC process that may be crucial for maintaining the structural and  
 CC functional integrity of nerve terminals.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Found in late  
 CC endosomes and lysosomes.

CC    -!- DOMAIN: A cysteine-rich N-terminal domain and a C-terminal domain  
 CC           containing a di-leucine motif necessary for lysosomal targeting  
 CC           are critical for mobilization of cholesterol from lysosomes.  
 CC    -!- PTM: Glycosylated.  
 CC    -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease  
 CC           type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lipid  
 CC           storage disorder, which affects particularly the brain, liver and  
 CC           spleen, and which is characterized by lysosomal accumulation of  
 CC           low density lipoprotein derived cholesterol. Clinical features  
 CC           include variable hepatosplenomegaly and severe progressive  
 CC           neurological dysfunction such as ataxia, dystonia and dementia.  
 CC           The age of onset can vary from infancy to late adulthood.  
 CC    -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease  
 CC           type D (NPD) [MIM:257250]; also known as Niemann-Pick disease  
 CC           without sphingomyelinase deficiency, or Nova Scotian type. Because  
 CC           of evidence from biochemical changes, lack of complementation, and  
 CC           linkage mapping to the same chromosome site, NPD and NPC1 are  
 CC           considered to be allelic disorders.  
 CC    -!- SIMILARITY: Belongs to the patched family.  
 CC    -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.

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 CC    -----

DR    EMBL; AF002020; AAB63982.1; -.  
 DR    EMBL; AF157379; AAD48006.1; -.  
 DR    EMBL; AF157365; AAD48006.1; JOINED.  
 DR    EMBL; AF157366; AAD48006.1; JOINED.  
 DR    EMBL; AF157367; AAD48006.1; JOINED.  
 DR    EMBL; AF157368; AAD48006.1; JOINED.  
 DR    EMBL; AF157369; AAD48006.1; JOINED.  
 DR    EMBL; AF157370; AAD48006.1; JOINED.  
 DR    EMBL; AF157371; AAD48006.1; JOINED.  
 DR    EMBL; AF157372; AAD48006.1; JOINED.  
 DR    EMBL; AF157373; AAD48006.1; JOINED.  
 DR    EMBL; AF157374; AAD48006.1; JOINED.  
 DR    EMBL; AF157375; AAD48006.1; JOINED.  
 DR    EMBL; AF157376; AAD48006.1; JOINED.  
 DR    EMBL; AF157377; AAD48006.1; JOINED.  
 DR    EMBL; AF157378; AAD48006.1; JOINED.  
 DR    EMBL; AF338230; AAK25791.1; -.  
 DR    EMBL; AF123046; AAF28875.1; -.  
 DR    EMBL; AF123045; AAF28875.1; JOINED.  
 DR    Genew; HGNC:7897; NPC1.  
 DR    MIM; 607623; -.  
 DR    MIM; 257220; -.  
 DR    MIM; 257250; -.  
 DR    GO; GO:0016021; C:integral to membrane; TAS.  
 DR    GO; GO:0005764; C:lysosome; TAS.  
 DR    GO; GO:0005624; C:membrane fraction; TAS.  
 DR    GO; GO:0005478; F:intracellular transporter activity; TAS.  
 DR    GO; GO:0015248; F:sterol transporter activity; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS.  
 DR InterPro; IPR004765; NP\_C type.  
 DR InterPro; IPR003392; Patched.  
 DR InterPro; IPR000731; SSD\_5TM.  
 DR Pfam; PF02460; Patched; 1.  
 DR TIGRFAMs; TIGR00917; 2A060601; 1.  
 DR PROSITE; PS50156; SSD; 1.  
 KW Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism;  
 KW Disease mutation.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 1278 NIEMANN-PICK C1 PROTEIN.  
 FT TRANSMEM 270 290 POTENTIAL.  
 FT TRANSMEM 351 371 POTENTIAL.  
 FT TRANSMEM 622 642 POTENTIAL.  
 FT TRANSMEM 655 675 POTENTIAL.  
 FT TRANSMEM 678 698 POTENTIAL.  
 FT TRANSMEM 760 780 POTENTIAL.  
 FT TRANSMEM 833 853 POTENTIAL.  
 FT TRANSMEM 1099 1119 POTENTIAL.  
 FT TRANSMEM 1125 1145 POTENTIAL.  
 FT TRANSMEM 1196 1216 POTENTIAL.  
 FT TRANSMEM 1228 1248 POTENTIAL.  
 FT DOMAIN 249 259 POLY-PRO.  
 FT DOMAIN 620 785 SSD.  
 FT SITE 1275 1278 DI-LEUCINE MOTIF.  
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 9.6%; Score 88.5; DB 1; Length 1278;  
 Best Local Similarity 25.7%; Pred. No. 12;  
 Matches 39; Conservative 25; Mismatches 51; Indels 37; Gaps 7;

Qy 46 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 105  
 ::||| : : : : | | | : : | : ||| || ||  
 Db 598 NLTISFTAERSIEDELNRESDSDF-----TVVISYAIMFLYISIALGH----IKSCRR 647  
 Qy 106 LFLVDD-----LVDSLKFVILMWVFTYVGALENGLTLLILALI-----SLF 146  
 | || | : | : ||:|:| |||:::| : :|  
 Db 648 L-LVDSKVSLGIAGILVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703  
 Qy 147 SIPVIYERHQ----VQIDHYLGLANKSVKDAM 174  
 : |:| : :| || | :|  
 Db 704 ILVQAYQORDERLQGETLDQQQLGRVLGEVAPSM 735

# RESULT 13

MDLB\_BUCBP

ID MDLB\_BUCBP STANDARD; PRT; 578 AA.

AC Q89A96;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Multidrug resistance-like ATP-binding protein mdlB.

GN MDLB OR BBP424.

OS Buchnera aphidicola (subsp. Baizongia pistaciae).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Buchnera.

OX NCBI\_TaxID=135842;





## RESULT 14

Y015\_MYCGE

ID Y015\_MYCGE STANDARD; PRT; 589 AA.  
AC P47261;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical ABC transporter ATP-binding protein MG015.  
GN MG015.  
OS Mycoplasma genitalium.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33530 / G-37;  
RX MEDLINE=96026346; PubMed=7569993;  
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,  
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,  
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,  
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,  
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,  
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;  
RT "The minimal gene complement of Mycoplasma genitalium.";  
RL Science 270:397-403(1995).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to the ABC transporter family. MsbA subfamily.  
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DR EMBL; U39680; AAC71231.1; -.  
DR PIR; F64201; F64201.  
DR HSSP; P13569; 1NBD.  
DR TIGR; MG015; -.  
DR InterPro; IPR003593; AAA\_ATPase.  
DR InterPro; IPR001140; ABC\_TM\_transpt.  
DR InterPro; IPR003439; ABC\_transporter.  
DR Pfam; PF00664; ABC\_membrane; 1.  
DR Pfam; PF00005; ABC\_tran; 1.  
DR ProDom; PD000006; ABC\_transporter; 1.  
DR SMART; SM00382; AAA; 1.  
DR PROSITE; PS50929; ABC\_TM1F; 1.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 1.  
KW Hypothetical protein; ATP-binding; Transport; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 9 29 POTENTIAL.  
FT TRANSMEM 66 86 POTENTIAL.  
FT TRANSMEM 161 181 POTENTIAL.  
FT TRANSMEM 251 271 POTENTIAL.

FT TRANSMEM 280 300 POTENTIAL.  
 FT TRANSMEM 303 323 POTENTIAL.  
 FT NP\_BIND 385 392 ATP (POTENTIAL).  
 SQ SEQUENCE 589 AA; 66126 MW; 0EA6A816DD3A3CC9 CRC64;

Query Match 9.3%; Score 86; DB 1; Length 589;  
 Best Local Similarity 22.7%; Pred. No. 8.8;  
 Matches 45; Conservative 40; Mismatches 71; Indels 42; Gaps 7;

QY 3 VDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 62  
 || :| :: :| : : || |||| ::| ||: | : | | : |  
 Db 48 VDSIY-----SLIYPTNLNVFIRLT---IVSVTVFVAYALIFVFNVAQNYVG-IKLYQ 96  
 QY 63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLF-----LVDDLVDSDL 116  
 :: :|||: : : : : : : : : || : | : |  
 Db 97 QTCATLRWKAYLKMQSMSTSFFDTQNGDLM SRLTNDMYNIDNLTQAGGQAIQSLFNIL 156  
 QY 117 KFAVLMWVFTYVGALENGLTLLILALISLFSIPVIYER----HQVQ----- 158  
 :||::: : | || :| ||| : || : : |||  
 Db 157 TTSVLIFLLSPVIAL---ISLSILATLITFSFAFLKKS KTSYSQVQNNLGDMSGYIEEVL 213  
 QY 159 ----IDHYLGLANKSVKD 172  
 : | | | : ||  
 Db 214 TNHKVVHVLKLQEI MIKD 231

# RESULT 15

YBZ7\_YEAST

ID YBZ7\_YEAST STANDARD; PRT; 296 AA.

AC P38279;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Hypothetical 33.5 kDa protein in MRPS9-YSW1 intergenic region.

GN YBR147W OR YBR1124.

OS *Saccharomyces cerevisiae* (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI\_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c;

RA Entian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,

RA Niegemann E., Schenk-Groeninger R., Servos J., Wehner E.,

RA Wolter R., Brendel M., Bauer J., Braun H., Dern K., Duesterhus S.,

RA Gruenbein R., Hedges D., Kiesau P., Korol S., Krems B., Proft M.,

RA Siegers K., Baur A., Boles E., Miosga T.,

RA Schaaff-Gerstenschlaeger I., Zimmermann F.K.;

RL Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- SIMILARITY: SOME, TO S.POMBE SPAC2E12.03C AND SPAC17C9.10.

CC

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DR EMBL; Z36016; CAA85105.1; -.  
DR PIR; S46018; S46018.  
DR GermOnline; 138690; -.  
DR SGD; S0000351; YBR147W.  
DR InterPro; IPR006603; CTNS.  
DR Pfam; PF04193; PQ-loop; 2.  
DR SMART; SM00679; CTNS; 2.  
KW Hypothetical protein; Transmembrane.  
FT TRANSMEM 13 33 POTENTIAL.  
FT TRANSMEM 45 65 POTENTIAL.  
FT TRANSMEM 69 89 POTENTIAL.  
FT TRANSMEM 164 184 POTENTIAL.  
FT TRANSMEM 200 220 POTENTIAL.  
FT TRANSMEM 239 259 POTENTIAL.  
FT TRANSMEM 263 283 POTENTIAL.  
SQ SEQUENCE 296 AA; 33496 MW; 50D65896A1BAFB43 CRC64;

Query Match 9.2%; Score 85.5; DB 1; Length 296;  
Best Local Similarity 29.3%; Pred. No. 4.7;  
Matches 41; Conservative 17; Mismatches 55; Indels 27; Gaps 7;

Qy 17 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY----KGVIAIQKS-DEGH--- 68  
| | : | | : : : | | | : | | : : | : : | |  
Db 61 VMGAMQNLLP----TMIILAAYYTLADLILLIQCMWYDKEKKSILQEVKKNVDPVHLPP 116  
  
Qy 69 -----PFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSD-- 115  
| | | | | | : | | : | | | | : |  
Db 117 ANPINETVLQDVFNEYEP LLPRIEEEDSQSYSSLELGR-TIVVKE-RENFENDELIVSGV 174  
  
Qy 116 LKFAVLMWVFTYVGALFNGL 135  
| : | | : | | | :  
Db 175 LIAGILSWYISYCSGLDNGI 194

Search completed: September 29, 2004, 18:14:38  
Job time : 3.70944 secs